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ALIGNMENTS

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WPI; 1999-371125/31.	Griffais R;	(GEST) GENSET.	17-DEC-1997; 97FR-0016034.	28-NOV-1997; 97FR-0015041.	04-NOV-1998; 98US-0107077.		27-NOV-1998; 98WO-IB01939.		10-JUN-1999.		WO9928475-A2.		Chlamydia trachomatis.	Synthetic.		bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.	nongonococcal uretritis; epidymitis; cervicitis; salpingitis; PCR primer;	paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis;	Vaccine; eye disease; conventional trachoma; nonendemic trachoma;		PCR primer used to amplify an ORF of Chlamydia trachomatis.		07-OCT-1999 (first entry)		AAZ05048;		AAZO5048 standard; DNA; 20 BP.

Disclosure; Genome

sequence of Chlamydia trachomatis

Page 1738; 1755pp; English.

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ID AAV0
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Matches 14; Conserv
This 5' primer is used with a 3' primer (see AAV07954) in the PCR amplification of Helicobacter, e.g. Helicobacter pylori, genomic DNA in order to obtain DNA (see AAV07921) encoding the unprocessed form of a 76 kDa polypeptide (see AAW073032) designated GHPO 1414. The isolated polynucleotide, and encoded polypeptide, can be used to develop vaccines for the treatment and prevention of Helicobacter
                                                                                                         Claim 5;
                                                                                                                                   New isolated Helicobacter polynucleotides - for the diagnosis, prevention and treatment infections and gastroduodenal diseases
                                                                                                                                                                                                 WPI; 1998-568251/48.
                                                                                                                                                                                                                            Al-Garawi A,
                                                                                                                                                                                                                                                                                                    01-APR-1997;
01-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, salpingitis, perihepatitis, bartholinitis; pneumopathy in breast feeding infants; and venereal lymphogranulomatosis. The polypeptides of the invention may be of use in treating these diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCR primers AAZ01426-Z06209 were used to amplify open reading frames (ORFS) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFS encode polypeptides (see AAY36724-Y37949) which can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye
                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
(INMR ) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS ET VACCINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GHPO 1414; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Helicobacter pylori polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                therapy; PCR;
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9.4e+02;
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Query Match Best Local Matches

Local Similarity

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Conservative

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Mismatches

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Indels

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0;

100.0%; 15.6%;

Score 14; Pred. No.

DB 19; . 9.3e+02;

Length. 26;

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                                                                    This 5' primer is used with a 3' primer (see AAV amplification of Helicobacter, e.g. Helicobacter DNA in order to obtain DNA (see AAV72001
                                                                                                                                                                                                                                                       01-APR-1997;
01-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                           GHPO
Sequence 26 BP; 15
                             ) encoding the unprocessed form of a 76 kDa polypeptide (see AAW73022) designated GHPO 386. isolated polypucleotide, and encoded polypeptide, can be used to develop vaccines for the treatment and prevention of Helicobacte.
                                                                                                                Claim 5; Page 137; 184pp; English.
                                                                                                                                               New isolated Helicobacter polynucleotides - used to develop for the diagnosis, prevention and treatment of Helicobacter
                                                                                                                                                                               WPI; 1998-568251/48
                                                                                                                                                                                                   Al-Garawi A,
                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC.
(INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS ET VACCINS
                                                                                                                                                                                                                                                                                                        08-OCT-1998
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Best Local
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                                                                                                                                                                                                                                                                                                             This 5' primer is used with a 3' primer (see AAV07939) in the PCR amplification of Helicobacter, e.g. Helicobacter pylori, genomic DNA in order to obtain DNA (see AAV07916) encoding the unprocessed form of a 76 kDa polypeptide (see AAW73027) designated GHPO 896. The isolated polypucleotide, and encoded polypeptide, can be used to develop vaccines for the treatment and prevention of Helicobacter
          Human genome; biallelic marker; high density disequilibrium map; genomic map; haplotype; phenotype; polymorphic base; genotyping; haplotyping; hybridisation; identification; characterisation; diagnosis; single nucleotide polymorphism; SNP; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GHPO 896; infection; gastritis;
therapy; PCR; primer; ss.
                                                               Human map-related biallelic marker SEQ ID NO:3195.
                                                                                    10-SEP-2001
                                                                                                         AAZ68842;
                                                                                                                             AAZ68842 standard; DNA;
                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                           Claim 5; Page 141; 184pp; English.
                                                                                                                                                                                                                                                                                                                                                                                              infections and gastroduodenal diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC.
(INMR ) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS ET VACCINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-APR-1997;
01-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9843479-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapy; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Helicobacter pylori polypeptide
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                                                                                                                                                                                   18
                                                                                                                                                                                               40 ttttcatgttttct 53
                                                                                                                                                                                   TTTTCATGTTTTCT
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                                                                                                                                                                                                                             14;
                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                           15.6%;
ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                  B₽;
                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     primer;
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97US-0831310.
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Pred. No.
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                                                                                                                                                                                                                                                                                  other;
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                                                                                                                                                                                                                           DB 19; I
9.3e+02;
hes 0;
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                                                                                                                                                                                                                                                Length 27;
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ID AAQ920
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AC AAQ920
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VS 418
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Best Local
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              US5418155-A
                                     Synthetic
                                                           antibody; oligonucleotide;
                                                                                                                       07-JAN-1996
                                                                                                                                                AAQ92084
                                                                                                                                                                       AAQ92084 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                              Sequence 47
                                                                                                                                                                                                                                                                                                                                                                                     N.B. The SEQ ID NOS 2852, and 3367, are not actually
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel biallelic markers
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23-NOV-1998;
                                                                         Luciferase;
                                                                                               Renilla reniformis luciferase DNA probe-1.
                                                                                                                                                                                                                                                                                                                                                                                                            treatment
                                                                                                                                                                                                                                                                                                                                                                                                                         effects from pharmaceutical agents acting on a disease as well as other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3;
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                                                                                                                                                                                                                                   43 AATGAAAGCAAGTG
                                                                                                                                                                                                                                                                                   Local Similarity
nes 14; Conserv
                                                                                                                                                                                                                                                         75 aatgaaagcaagtg
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                                                                                                                                                                                                                                                                                                                                                                        present invention.
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                                                                                                                                                                                                                                                                                                                                                                                  are not actually given a sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Blumenfeld
                                                                                                                                                                                                                                                                                                                                               BP; 13 A; 13 C; 6
                                                                         enzyme;
                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                       (first entry)
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98US-0109732
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                                                                         bioluminescence; luminescence; label; DNA probe;
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Pred. No.
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9.1e+02;
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RESULT
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Best Local Similarity
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20-AUG-1992;
17-JUN-1993;
14-DEC-1993;
Page 1737; Disclosure; 1912pp; English
                                             Genome sequence of Chlamydia pneumoniae
                                                                                                  WPI; 1999-357842/30.
                                                                                                                                                                                                                                                  04-NOV-1998;
21-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Respiratory disease; pneumonia; bronchitis; heart disease; sarcc sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This 17-mer oligonucleotide DNA probe, along with Probe-2 (AAQ92085) are used to screen an R. reniformis cDNA library to isolate cDNA encoding Renilla luciferase. The luciferase was then expressed using E. coli.
                                                                                                                                                                                                  (GEST ) GENSET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCR primer used to amplify an ORF of Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig. 4; 18pp; English.
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                                                                                                                                                                                                                                                                                                                         20-NOV-1998;
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luminescent tag, partic
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93US-0079700.
93US-0167650.
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97FR-0014673
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in bio-luminescence assays and for the prodn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 G;
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2.8e+03;
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AAH27610
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                                                                                                                                                                                                                                                                                                                                                                           PR XX
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Best Local
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                                          The invention relates to an isolated polypeptide of human lipoprotein 105 containing a cytochrome c structural domain. The polypeptide comprises a 951 amino acid sequence given in the specification, or its fragment, analogue or derivative. The polypeptide and encoded polypucleotide are useful in the diagnosis and treatment of malignant tumours, haemopathy, HIV infection, immunological diseases and various inflammatory diseases. The present sequence is a primer which was
                                                                                                                                                                                                                         Human lipoprotein 105 containing cytochrome c structural domain and encoded polynucleotide, applicable in diagnosis and treatment of malignant tumor, hemopathy, HIV infection, immunological diseases and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           frames and other nucleic acid sequences from the genome of Chlamydia pneumoniae (see AAX91990). C. pneumoniae causes respiratory disease such as pneumonia and borochitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encode by the open reading frames of the C. pneumoniae genome (see AAX93684-AAX93879) can be used in immunogenic compositions as vaccines. Vectors
                                                                                                                                                                                                                                                                                             WPI; 2001-374839/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAH27610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
                           used to isolate the polynucleotide encoding the polypeptide of the
                                                                                                                                                                            Example 2; Page 12; 40pp; Chinese.
                                                                                                                                                                                                               various inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                          27-NOV-2000; 2000WO-CN00503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200140483-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human lipoprotein 105 PCR primer 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH27610 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20 BP; 5 A; 5 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX91991-X97517 represent PCR primers used to amplify open
                                                                                                                                                                                                                                                                                                                                                          (BIOR-) BIOROAD GENE DEV LTD SHANGHAI.
                                                                                                                                                                                                                                                                                                                                                                                           29-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      haemopathy; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; lipoprotein 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .mmunomodulatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77 tgaaagcaagtgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity les 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       uman immunodeficiency virus; HIV; immunological disease; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                           99CN-0124136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytochrome c structural domain; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytostatic; anti-HIV; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ΒP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 20; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 20;
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Length 23;

Query Match

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RESULT
AAH55939
                                                                       The present invention describes a method (M1) of determining an C individual's predisposition to epilepsy and/or development of epilepsy. C as well as predicting the individual's response to medication. The C method comprises determining the genotype of at least one gene selected CC from SCNIA, SCNIA or SCNIA, or a DNA variant, equivalent, or mutation CC which shows a linkage disequilibrium. SCNIA, SCNIA and SCNIA are all C sodium channel genes located on chromosome 2. The idiopathic generalised CC epilepsy (IGE) gene is more specifically localised on chromosome C q23-q31. Compounds identified as modulators of the biological activity CC of SCNIA, SCNIA or SCNIA proteins or genes, are useful for treating CC epilepsy or other neurological disorders. They have anticonvulsant and CC neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to CC AAB99679 represent SCNIA, SCNIA, and SCNIA cDNAs, gene fragments, PCR CC primers, oligonucleotides and proteins given in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qy
 Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
                                                                                                                                                                                                                                                                                                                           Example 3; Fig 2; 268pp; English.
                                                                                                                                                                                                                                                                                                                                                       disequilibrium
                                                                                                                                                                                                                                                                                                                                                                   Determining a predisposition to epilepsy and/or development of epilepsy comprises determining the genotype of SCNIA, SCN2A and/or SCN3A, or a DNA variant, equivalent, or mutation which shows a linkage
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rouleau
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-NOV-2000; 2000WO-CA01404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200138564-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnosis; mutation; chromosome 2q23-q31; neurological disorder; anticonvulsant; neuroprotective; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human SCN1A PCR-SSCP PCR primer SEQ ID NO:183.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH55939;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYMC-) UNIV MCGILL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 ttttatgttttca 45
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                                                                                                                                                                                                                                                                                                                                                                                                                              2001-355945/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GA,
                                                                       24
                                                                       BP;
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LaFreniere RG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0167623
                                                                       N
                                                                       A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.4%; 5c-
100.0%; Pro
                                                                       5 C;
             14.4%; Score 13; 100.0%; Pred. No.
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 0;
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Pred.
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                                                                     14 T;
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  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 νő
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                                                                       0
                                                                       other;
             DB 22;
2.8e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22; I
2.8e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cossette
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 0;
                          Length 24;
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AAQ68537/c
ID AAQ68537 standard; cDNA; 26
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                                                                                                                                         RESULT 11
                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                        Query Match,
Best Local S
                          Human; mitochondrial genome; single nucleotide Alzheimer's disease; mtDNA; PCR primer; ss.
                                                                              14-FEB-2001
                                                                                                                                                                                                                                                                                             The N-terminal sequence of a 33kD delta-endotoxin isolated from B.thuringiensis EMCC0075 (NRRL B-21019) or EMCC0076 (NRRL B-21020) was determined (see AAR59764). Based on this sequence a 26mer oligonucleotide was designed for use as a probe (AAQ68537) for cloning
                                                         Alzheimer's disease-linked mitochondrial SNP PCR primer #12
                                                                                                  AAC67312;
                                                                                                                    AAC67312 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthétic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ68537;
                                                                                                                                                                                                                                                                Sequence 26 BP; 13 A; 2 C;
                                                                                                                                                                                                                                                                                     the delta-endotoxin
                                                                                                                                                                                                                                                                                                                                                  Example 9;
                                                                                                                                                                                                                                                                                                                                                                      Coleopteran
                                                                                                                                                                                                                                                                                                                                                                             New Bacillus thuringiensis strains - which produce new delta-endotoxin cpds used for the control of Lepidopteran and
                                                                                                                                                                                                                                                                                                                                                                                                                                 Adams LF, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09413785-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B.thuringiensis 33kD delta-endotoxin N-terminal probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NOVO ) NOVO-NORDISK ENTOTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lepidoptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insecticidal
                                                                                                                                                                    16 AATTTTTATGTTT
                                                                                                                                                                                          30 aatttttatgttt 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 tttatgttttcat
                                                                                                                                                                                                               Local Similarity es 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                  Page 26; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                      insect pests.
                                                                                                                                                                                                                Conservative
                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92US-0991073.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93WO-US12144.
                                                                                                                                                                         4
                                                                                                                                                                                                                                                                                                                                                                                                                                 Lufburrow PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46
                                                                                                                                                                                                                                                                                    gene.
                                                                                                                                                                                                                        14.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thuringiensis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       delta-endotoxin; crystal; Coleoptera;
                                                                                                                       26
                                                                                                                                                                                                                         .0%;
                                                                                                                       ВP
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                                                                                                                                                                                                                        Score 13;
Pred. No.
                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Thomas MD
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                                                                                                                                                                                                                        DB 15;
2.8e+03;
                                                                                                                                                                                                                0;
                                    polymorphism; SNP;
                                                                                                                                                                                                                                 Length 26
                                                                                                                                                                                                               Indels
                                                                                                                                                                                                               0;
                                                                                                                                                                                                               Gaps
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Homo sapiens

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                          Matches
                     WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diagnosing a subject at the risk for or having Alzheimer's disease comprises determining at least one single nucleotide polymorphism in mitochondrial DNA associated with the disease in the sample from the subject
Diagnosing a subject at the risk for or having Alzheimer's disease
                                         Herrnstadt C,
                                                                                   20-APR-1999;
22-OCT-1999;
                                                                                                                                                                                                                                Alzheimer's disease-linked mitochondrial SNP PCR primer #42
                                                                                                                                                                                                                                                                          AAC67342;
                                                                                                                                                                                                                                                                                              AAC67342 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a novel method for determining the risk of or diagnosing Alzheimer's disease using single nucleotide polymorphisms (SNPs) present in an individual's mitochondrial DNA (mtDNA). In addition, the SNPs identified can be used to identify agents suitable for use in treating Alzheimer's disease. Sequences AAC67301-C67610 are PCR primers used to demonstrate the method of the
                                                             (MITO-) MITOKOR
                                                                                                                19-APR-2000;
                                                                                                                                     26-OCT-2000
                                                                                                                                                         WO200063441-A2
                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                    Alzheimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; Page 34; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Herrnstadt C,
                                                                                                                                                                                                  Human; mitochondrial
Alzheimer's disease;
                                                                                                                                                                                                                                                      14-FEB-2001
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22-OCT-1999;
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nes 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                     37 atgttttcatgtt
                                                                                                                                                                                                                                                                                                                   12
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                     2000-672748/65
                                                                                                                                                                                                                                                                                                                                                2000-672748/65
                                                                                                                                                                                                                                                                                                                                                                                                                                            BP; 8 A;
                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                2000WO-US10906
                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000WO-US10906
                                         Davis
                                                                                  99US-0130447.
99US-0160901.
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99US-0160901
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                                                                                                                                                                                                                                                                                              DNA;
                                                                                                                                                                                                                                                                                                                                                 19
                                                                                                                                                                                                                                                                                                                                                                     49
                                                                                                                                                                                                  genome;
mtDNA; I
                                                                                                                                                                                                                                                                                                                                                                                                  14.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                           2 C;
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                                                                                                                                                                                                                                                                                              ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>ن</u>
                                                                                                                                                                                                  ; single nucleotide polymorphism;
PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                   Score 13;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                            11 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  DB 21; 1
2.8e+03;
                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                             Length 26;
                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                             SNP;
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RESULT 1
AAV07957/
   CCCCCCXXXIII
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Best Local Similarity
This 5' primer was used with a 3' primer (see AAV07958) in the PCR amplification of Helicobacter pylori strain ORV2001 genomic DNA in order to obtain DNA (see AAV72001) encoding a 76 kDa polypeptide (see AAW73022) designated GHPO 386. The primer pair includes a 5' clamp and BamHI and XhoI restriction enzyme recognition sequences for cloning purposes. The PCR product was ligated into vector pET28a, and recombinant polypeptide was expressed as a histidine-tagged fusion protein in E. coli host cells. The polypeptide can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of or diagnosing Alzheimer's disease using sligle nucleotide polymorphisms (SNPs) present in an individual's mitochondrial DNA (mtDNA). In additon, the SNPs identified can be used to identify agents suitable for use in treating Alzheimer's disease. Sequences AAC67301-C67610 are PCR primers used to demonstrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                  GHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   comprises determining at least one single nucleotide polymorphism mitochondrial DNA associated with the disease in the sample from \ensuremath{\mathsf{t}}
                                                                                                                      Example 3.B;
                                                                                                                                                                                            WPI; 1998-568251/48
                                                                                                                                                                                                                   Al-Garawi A,
                                                                                                                                                                                                                                                                             01-APR-1997;
                                                                                                                                                                                                                                                                                       01-APR-1997;
                                                                                                                                                                                                                                                                                                                31-MAR-1998;
                                                                                                                                                                                                                                                                                                                                       08-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                       PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-FEB-1999
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                                                                                                                                                                   New isolated Helicobacter polynucleotides -
                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC.
(INMR ) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS ET VACCINS
                                                                                                                                                                                                                                                                                                                                                             WO9843479-A1
                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                   Helicobacter pylori
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                                                                                                                                                        the diagnosis, prevention
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                                                                                                                                                                                                                                                                                                                                                                                                                      primer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                infection;
                                                                                                                                           agnosis, prevention and treatment and gastroduodenal diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                    Page 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first
                                                                                                                                                                                                                  Kleanthous H,
                                                                                                                                                                                                                                                                            97US-0834666.
97US-0831310.
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100.0%;
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                                                                                                                      English.
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2 8e+03;
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                                                                                                                                                       of Helicobacter
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RESULT 14
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Matches 13
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Best Local
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                                                                                                                                     Nucleic acid encoding the human azoospermia factor, and probes and antibodies specific for the sequence and encoded polypeptide - may be used in the clinical diagnosis of male infertility
                                                                       The intron/exon boundaries of a human YRRM gene encoding azoospermia factor were detd. by comparison of the sequences found in cosmid A5F DNA obtd. from a Y-chromosome specific colibrary and the cDNA clone MK5 (AAQ87655) obtd. from an adult
                                                                                                                      Disclosure; Fig 3; 40pp; English.
                                                                                                                                                                             WPI;
                                                                                                                                                                                              Chandley AC,
                                                                                                                                                                                                                                  07-JUL-1994;
22-OCT-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                (MEDI-) MEDICAL RES
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Local Similarity
nes 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31 TTTCATGTTTTCT 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                              34
                                                                                                                                                                                                                                                                                                                                                                                                                                         factor;
                                              ВP;
 Conservative
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                                                                                                                                                                                             Cooke HJ,
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93GB-0021857.
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/note= "Represents
18.34
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                                                                                                                                                                                                                                                                                                                                                                                                                                        AZF;
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         14.4%;
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Pred. No.
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ore 13; DB 16; red. No. 2.7e+03; Mismatches 0;
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2.7e+03;
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Indels
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RESULT 15
AAF61207/c
                                                                                                           This invention describes a novel recombinant RNA molecule (I), at least CC partly translatable in a target cell which comprises: (a) the conditions genome (A) of Group B Coxsackie virus (CVB), particularly construction and (b) at least one foreign gene (II) that can be developed convention also describes (1) a recombinant infectious virions (V), CC derived from (A) and containing (I); (2) a plasmid vector containing the construct for complementing the coding sequence exchanged by (I); (4) constructs of (3); (7) a kit containing the vector of (2) or the helper constructs of (3); (8) a DNA molecule (IV) containing at least one coding sequence for (I); (9) a kit containing (IV); (10) a kit for performing constructs of (3); (11) a DNA construct that encodes (I) and can persist (and is transcribed) in target cells, but is preferably not replicable; (12) a recombinant virus (RV), particularly adeno or retro, that encodes (I) and is expressed after infection into a target cell to produce a cytoplasmic replicon that is continuously replenished; (13) producing crecombinant DNA viruses or virions having a DNA genome that lacks a crecombinant vector system with a RNA genome. The products of the crecombinant vector system with a RNA genome. The products of the crecombinant vector system with a RNA genome. The products of the crecombinant vector system with a RNA genome. The products of the crecombinant vector system with a RNA genome. The products of the crecombinant vectors service activity and can be used for gene therapy. (C) is used to produce gene therapy vectors, particularly plasmids or congenital or acquired. (I) particularly vectors derived from DNA viruses, articularly vectors derived from DNA viruses.
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        particular gene sequences, particularly vectors derived from DNA virus vectors based on (I) transfer genes to cardiac myocytes without immunological or other side effects. The RNA genome can replicate, providing efficient gene transfer and long-term expression of the therapeutic gene. CBV is naturally trophic for heart muscle and since
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant RNA comprising heterologous gene in Coxsackie viral genome, useful in gene therapy, specifically for targeting of cardiac myocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Coxsackievirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene therapy; infectious virion; cardioactive; cardiac muscle; trophic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-AUG-1999;
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life cycle,

danger that

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RESULT 1
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                                                                  The present sequence is that of primer 3A, which is 1 of a set of C a nested primers (see also AAF90561 and AAF90562) homologous to C the 3' DS3 region of Dissociation transposon. Arbitrary degenerate Primers (see AAF90551-56) were used to prime Arabidopsis thaliana C genomic DNA flanking the site of a Ds transposon insertion. The C degenerate primers were used in combination with 2 sets of 3, nested, transposon-specific primers homologous to the DS3 region or DS5 region (see AAF90557-59) of the Ds element, which lie at the C outermost ends of the transposon. Low- and high-stringency PCR amplifications were performed using the TAIL-PCR produced. DNA 1C fragments were produced which corresponded to the genomic DNA that C was directly adjacent to the transposon insertion. Sequence analysis of PCR products from tagged seedling lethal lines E71158, C most of the sessential for Arabidopsis seedling growth and development. The essentiality of the genes provides a means of discovering new herbicides. Screening assays for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         망
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Best Local
                            discovering new herbicides. Screening assays for identifying inhibitors that are potential herbicides are provided. The invention is also applied to the development of herbicide tolerant plants, and plant tissues, seeds and cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ET1158 gene; GT6839 gene; ET5262 gene; herbicide tolerance; transgenic plant; Dissociation; transposon; maize; PCR pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               foreign genes will become integrated in the target cell genome. By using (II) to replace part of the viral coding region, large (II) sequences may be accommodated. (I) is easily packaged in CVB capsid proteins.
                                                                                                                                                                                                                                                                                                                                                                                                    New herbicide target genes encoding ET5262 activity, for identifying an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wegrich Glover L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-DEC-2000; 2000WO-EP12748
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SYGN ) SYNGENTA PARTICIPATIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 aaattatttcaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAATTATTTCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transposon 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Budziszewski GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.4%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        flanking nested primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                    proteins having ET1158, GT6839 or inhibitor of protein activity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Levin JZ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           crop protection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            herbicide; screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22;
2.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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Sequence 36

BP; 6 A; 4 C;

11 G;

15 T; 0 other;

RESULT

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DЬ
                      Qy
                                   Query Match
Best Local Similarity
Whiches 13; Conserv
                                                                                                               Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 17
AAT34130/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                             primers MW093 (AAT34127) and MW110 (AAT34128) were used to generate a 100 bp PCR fragment, PCR-HTIV18, contg. the 13L promoter fused to the 5'-end of the HTLV-I envelope gene, using pMM102 as template. Primers MW113 (AAT34129) and MW116 (AAT34130) were used to generate 1,500 bp PCR fragment, PCR-HTIV21, contg. the 3' end of the 13L promoter fused to the entire HTLV-I envelope gene, using p17-SST as template. MW093 and MW116 were then used as to amplify PCR-HTIV18 and PCR-HTIV21. The 13L-promoted envelope gene was cloned between canarypox virus C5 flanking arms and also between vaccinia HA flanking arms, and a NYVAC recombinant expressing HTLV-I env was generated. This effectively primed protective immune responses
                                                                                                              Sequence
                                                                                                                                       against retrovirus challenge.
                                                                                                                                                                                                                                                                                                                                      Attenuated recombinant pox-viruses expressing HTLV antigens - safe vaccination against HTLV infection, and for therapy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Avipox virus; poxvirus; vector; vaccine; attenuation; HTLV-I human lymphotropic virus; safety; ALVAC; NYVAC; primer; PCR; polymerase chain reaction; vaccinia virus; retrovirus; ss.
                                                                                                                                                                                                                                                                                                    Example
                                                                                                                                                                                                                                                                                                                                                                                                       Franchini G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT34130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT34130 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                             (VIRO-) VIROGENETICS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9621727-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  I3L promoter-HTLV-I fusion primer MW116
                       26 ctgtaattttat
25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 tatgttttcatgt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 tatgttttcatgt 48
CTGTAATTTTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                   12; Page 96; 165pp; English
                                                                                                               38
                                                                                                               B₽;
                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first
                                                                                                                                                                                                                                                                                                                                                                                                       Gallo RC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       95US-0372664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96WO-US00547
                                                                                                               15
                                                                                                              A; 6
                       38
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w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.4%;
                                                             100.0%;
                                                                         14.4%;
                                                                                                              C; 8
                                                                                                                                                                                                                                                                                                                                                                                                       Paoletti E,
                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                            Score 13;
Pred. No.
                                                                                                              G; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 13;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                             Mismatches
                                                                                                               T; 0 other
                                                                                                                                                                                                                                                                                                                                                                                                     Tartaglia
                                                            DB 17;
. 2.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22;
2.7e+03;
                                                0;
                                                                      Length 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 36;
                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                     tor
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                0;
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RESULT 1
AAQ35353/
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ID AAQ35630 standard; DNA; 39
                                                                                                                                                                    Query Match
Best Local S
Matches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-MAR-1991;
11-JUN-1991;
06-MAR-1992;
                                                                                                                                                                                                                                                    NYVAC recombinants expressing HIV-2 gene products. NYVAC is a Copenhagen vaccine strain of vaccinia virus which has been modified by deletion of six non-essential regions of the genome encoding known or potential virulence factors. The deletion loci were engineered as recipient loci for the insertion of foreing genes. The HIV-2 env sequence was isolated in two portions by polymerase chain reaction (PCR). These fragments were then ligated also by PCR. The HIV-2 gpl20 gene was also isolated by PCR. These HIV-2 genes were transfected into NYVAC which could then be cultured in Vero cells. The envelope proteins were found to be present on the cell surface of cells transformed with the recombinant NYVAC. See AAQ35501-864.
                                                    ,T 19
:353/c
AAQ35353 standard;
          18-MAY-1993
                                 AAQ35353;
                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                           The sequences given in AAQ35624-32 were used in the construction of
                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 156; 455pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                              HIV, HSV, EBV, CMV, mumps etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vaccine comprises recombinant, attenuated vaccinating against viral infections such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1992-331718/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Riviere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cox WI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9215672-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cell surface;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NYVAC; recombinant; HIV-2; Copenhagen vaccine; vaccinia virus; virulence factors; deletion loci; recipient loci; env; amplify; PCR; polymerase chain reaction; gp120; transfection; Vero cells; envelope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIV-2 env 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Limbach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (VIRO-) VIROGENETICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-FEB-1993
                                                                                                                     25
                                                                                                                                              26
                                                                                                                                  ctgtaattttat 38
                                                                                                                     CTGTAATTTTAT 13
                                                                                                                                                                      l Similarity
13; Conserv
                                                                                                                                                                                                                                 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            De Taisne C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Norton EK,
Tartaglia J,
                                                                                                                                                                                                                                 ВP;
                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fragment primer HIV2B2.
        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91US-0666056.
91US-0713967.
92US-0847951.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92WO-US01906
                                                                                                                                                                                                                                 15
                                                                                                                                                                                                                                Α;
                                                         DNA;
                                                                                                                                                                                14.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , Francis J, Ge
EK, Paoletti E,
a J, Taylor J;
                                                                                                                                                                                                                                6
                                                         39
                                                                                                                                                                                                                                Ç;
                                                                                                                                                                                                                                 7
                                                         ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ВP
                                                                                                                                                                      0;
                                                                                                                                                                               Score 13;
Pred. No.
                                                                                                                                                                                                                                <u>G</u>
                                                                                                                                                                                                                                11 T; 0 other;
                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gettig RR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Perkus ME,
                                                                                                                                                                    DB 13; I
2.7e+03;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         pox-virus - use for
as rabies, hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Johnson GP;
                                                                                                                                                                                           Length 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pincus SE;
                                                                                                                                                                     Indels
                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                      В,
                                                                                                                                                                    Gaps
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X P X P X S X X X X E
                                                                                                                                                                                                                                                                                             В
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                                                                                                                                                                                                                                                                                                                                                                                             AAA99138
                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                       OmpT protease; cleavage; fusion protein; membrane protease; natriuretic; Escherichia coli; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                    The 3' portion of the HIV-2 env gene was derived by PCR. In this reaction a 270 bp fragment was amplified using oligonucleotides HIV2B1 and HIV2B2 using pISW-SNP as the prod. was digested with BanHI and XbaI to yield a 150 bp fragment which was engineered to contain a TSNT sequence known to be recognised as vaccinia virus early transcription termination signal, following
                     04-MAR-1999;
                                         03-MAR-2000;
                                                               08-SEP-2000
                                                                                                                    Escherichia
                                                                                                                                                                      Plasmid pOmpTTc PCR primer SEQ ID NO:15
                                                                                                                                                                                             19-JAN-2001
                                                                                                                                                                                                                                        AAA99138 standard;
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 39
                                                                                   WO200052193-A1
                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                 See also AAQ35328-437.
                                                                                                                                                                                                                                                                                                                                                                                                                             the termination codon TAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 4; Page 52; 159pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified recombinant virus with inactivated non-essential genetic functions - comprises e.g. vaccinia or avipox virus, used as HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1993-018128/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (VIRO-) VIROGENETICS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-JUN-1991;
11-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9222641-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immunodeficiency virus; amplification; env;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCR primer HIV2B2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-JUN-1992;
                                                                                                                                                                                                                                                                                                                                       Local Similarity
nes 13; Conserv
                                                                                                                                                                                                                                                                                             25
                                                                                                                                                                                                                                                                                                                 26 ctgtaatttttat
                                                                                                                                                                                                                                                                                             CTGTAATTTTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Paoletti E,
                                                                                                                   coli.
                                                                                                                                                                                                                                                                                                                                                                                            BP; 15 A; 6 C; 7
                                                                                                                                                                                                                                                                                                                                        Conservative
                                         2000WO-JP01309.
                                                                                                                                                                                            (first entry)
                    99JP-0057731.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91US-0715921.
92US-0897382.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92WO-US05107
                                                                                                                                                                                                                                        DNA;
                                                                                                                                                                                                                                                                                             13
                                                                                                                                                                                                                                                                                                                 38
                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tartaglia
                                                                                                                                                                                                                                         39
                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                  Score 13; DB 14;
Pred. No. 2.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                            с;
                                                                                                                                                                                                                                                                                                                                                                                            11 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J,
                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                           Length 39;
                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISSY strain;
                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SS
                                                                                                                                                                                                                                                                                                                                       Gaps
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(SUNR) SUNTORY LTD

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converting the sites of polypeptides by CompT protease by preventing cleavage at unwanted sites by converting the amino acid residue at position +1 to the site is Lys or Arg), and/or converting the residue at converting the site is Lys or Arg), and/or converting the residue at converting the residue at position -4 and/or -6 to a specifically defined amino acid. Also described is a method for the fission of a fusion protein to give a convertine has a linker peptide inserted between the desired polypeptide polypeptide inserted between the desired polypeptide and the other part of the fusion protein. The fusion protein may be converted by expression of DNA encoding in a suitable host cell such as Escherichia coli. OmpT protease is a membrane protease of Escherichia coli which cleaves peptide chains at a two-residue sites in which both cresidues are basic amino acids such as arginine or lysine. The methods con be used for the efficient preparation of undegraded desired polypeptides such as natriuretic peptide by OmpT protease cleavage after recombinant expression as a fusion protein. AAA99177 and the present invention.
  RESULT 21
AAQ48717/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local s
Matches 13
 Expression with plasm
                                           WPI; 1993-298916/38
                                                                                                06-JUN-1990;
                                                                                                                          05-JUN-1991;
                                                                                                                                                      24-AUG-1993.
                                                                                                                                                                                JP05211866-A
                                                                                                                                                                                                                                       Mansonia;
                                                                                                                                                                                                                                                                 Caulobacter;
                                                                                                                                                                                                                                                                                                                                                                              AAQ48717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Controlled cleavage of peptides by OmpT protease by amino acid substitution for ensuring cleavage only at desired site in fission of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Okuno K,
                                                                     (SILM-)
                                                                                                                                                                                                                                                    Bacillus
                                                                                                                                                                                                                                                                                            Insecticidal
                                                                                                                                                                                                                                                                                                                        25-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                       21
                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 ctgtaattttat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
ession of insecticidal protein - by transforming Caulobacter plasmid contg. gene coding for insecticidal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ctgtaattttat
                                                                     SILMARAN
                                                                                                                                                                                                                                     sphaericus; larva;
; Aedes; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39
                                                                                                                                                                                                                                                                                                                                                                              standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yabuta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.48; ilarity 100.08; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP; 8 A; 9 C;
                                                                                                                                                                                                                                                  plasmid; insecticidal protein; Bacillus thuringiensis;
aericus; larva; mosquitoe; Culex; Anopheles; Psorophoa;
                                                                                                                                                                                                                                                                                         protein gene 3'
                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                               90JP-0148444
                                                                                                                          91JP-0160963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ĭ
                                                                   so
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 13;
Pred. No.
                                                                                                                                                                                                                                                                                           primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 21; 1
2.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 39;
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RESULT 22
AAZ61322/c
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Best Local
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                                                                                                                                                                                                                                                                                           03-AUG-1998;
03-AUG-1998;
15-DEC-1998;
29-APR-1999;
11-JUN-1999;
         Primers AAZ61218-45 were used to construct a synthetic Streptomyces hygroscopicus bar gene. The bar gene encodes phosphinothricin acetyltransferase, which provides protection from phosphinothricin toxicity. The synthetic gene has improved containment and enhanced expression in plant plastids, and is used to produce recombinant DNA constructs of the invention. The specification describes recombinant DNA constructs for expressing heterologous proteins (e.g. bar gene product) in the plastids of higher plants. The DNA constructs comprise a 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Two primers (AAQ48716-17) are described for the isolation of Bacillus thuringiensis israelensis DNA. The sequence of one 27-mer primer (AAQ48716), however is missing from the specification. Caulobacter transformed with a plasmid contg. a gene encoding insecticidal protein derived from Bacillus thuringiensis or Bacillus sphaericus will proliferate in aq. environment. They may be consumed by larvae of mosquitoes and are lethal to
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces hygroscopicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ61322 standard; DNA; 40
                                                                                                                               Example 7; Page 69; 164pp; English.
                                                                                                                                                          New recombinant DNA constructs, heterologous protein in plastids leader sequence and a downstream
                                                                                                                                                                                                               WPI; 2000-205525/18
                                                                                                                                                                                                                                                                    (RUTF ) UNIV
                                                                                                                                                                                                                                                                                                                                                                             03-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Culex, Anopheles, Psorophoa, Mansonia and Aedes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity hes 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene; phosphinothricin acetyltransferase; phosphinothricin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression; vaccine;
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                                                                                                                                                                                                                                         Kuroda H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                    RUTGERS
                                                                                                                                                                                                                                                                                           98US-0095163.
98US-0095167.
98US-0112257.
99US-0131611.
99US-0138764.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     construct a synthetic bar
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100.0%;
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                                                                                                                                                                                                                                         Khan MS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               haemoglobin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 13;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Japanese
                                                                                                                                                                                                                                                                    JERSEY.
                                                                                                                                                          for expressing high levels of 
is of higher plants, includes promoter, a 
im box element -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
promoter
                                                                                                                                                                                                                                                                                                                                                                                                            197,
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2.7e+03;
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Best Local
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                                                                                                                                                                                                                                                                                                                         03-AUG-1998;
03-AUG-1998;
15-DEC-1998;
29-APR-1999;
                                         Primers AAZ61218-45 were used to construct a synthetic Streptomyces hygroscopicus bar gene. The bar gene encodes phosphinothricin acetyltransferase, which provides protection from phosphinothricin toxicity. The synthetic gene has improved containment and enhanced expression in plant plastids, and is used to produce recombinant DNA constructs of the invention. The specification describes recombinant DNA
constructs for expressing heterologous proteins (e.g. bar gene product) in the plastids of higher plants. The DNA constructs comprise a 5' regulatory region which includes a promoter element, a leader sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   heterologous protein. The chimeric regulatory region enhances translational efficiency of an mRNA molecule encoded by the DNA construct. The DNA constructs are used for producing transformed monocot and dicot plants having high levels of heterologous protein expression. They can be used to drive expression of proteins with agronomic, industrial or pharmaceutical importance, including production of vaccines, healthcare products like human haemoglobin, industrial or household enzymes. Plants which can be transformed with the constructs of the invention include maize, millet, sorghum, sugar cane, rice,
                                                                                                                                            Example
                                                                                                                                                                                    heterologous
                                                                                                                                                                                                New recombinant DNA constructs,
                                                                                                                                                                                                                                                        Maliga
                                                                                                                                                                                                                                                                                 (RUTF ) UNIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bar gene; phosphinothricin acetyltransferase; phosphinothricin toxicity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   downstream box element operably linked to a coding region of
                                                                                                                                                                      logous protein in plastids sequence and a downstream
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         barley, oat, rye or turf grass.
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                                                                                                                                          7; Page 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                       Kuroda H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP; 19 A; 6 C; 5 G;
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                                                                                                                                                                                                                                                                                  RUTGERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hygroscopicus
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99US-0131611.
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98US-0095167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30
                                                                                                                                          164pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vaccine; haemoglobin; enzyme; primer; ss
                                                                                                                                                                                                                                                                                  STATE NEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.4%;
                                                                                                                                                                                                                                                     Khan
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                                                                                                                                          English.
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               synthetic
                                                                                                                                                                                                                                                                                    JERSEY.
                                                                                                                                                                   for expressing high levels of s of higher plants, includes pm box element -
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No.
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2.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bar gene
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                                                                                                                                                                                 promoter,
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RESULT 24
AAV5109/c
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XX Claim
XX
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Best Local Similarity
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                                                                                                                                                                                                                                                     Brassica
- useful
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                                                                         polymorphic marker. This sequence can be used in the construction of allele-specific primers and probes for amplification or hybridisation, e.g. to determine common or disparate ancestry between 2 or more plant
                                                                                                                                                  This DNA sequence is a region of a Zea mays genome which contains
                                                                                                                                                                                                      Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                               Landry
                                                                                                                                                                                                                                                                                                                                                                                                                                 (AFFY-) AFFYMETRIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            progeny; back-cross; hybrid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polymorphic marker; allele-specific; primer; probe; hybridisation; plant; hybrid certification; genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 40
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                                                                                                                                                                                                                                                                                                                                                                               BS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13;
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                                                                                                                                                                                                   Page 43; 65pp; English
                                                                                                                                                                                                                                                  species allele-specific for plant breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B₽;
                                                                                                                                                                                                                                                                                                                                                                             Lemieux B,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /replace=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note≃ "polymorphism"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ancestry; maize; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 13;
Pred. No.
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to monitor the genetic contribution of an ancestral plant, to progeny of proprietary plants, in certification of a hybrid planentify the progeny of a back-crossed plant with an ancestral

to trace the d plant or to

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AAV51011/c
ID AAV510
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Best Local Similarity
Matches 13; Conserv
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This DNA sequence is a region of a Zea mays genome which contains a polymorphic marker. This sequence can be used in the construction of allele-specific primers and probes for amplification or hybridisation, e.g. to determine common or disparate ancestry between 2 or more plants,
                                                                                                                                                                                                                                                                                                                Sequence 41
                                                                                                                                                                                                                                                                                                                                                                               to monitor the genetic contribution of an ancestral plant, to i
progeny of proprietary plants, in certification of a hybrid pla
identify the progeny of a back-crossed plant with an ancestral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1;
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02-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               species allele-specific oligonucleotide probes and primers for plant breeding % \left( 1\right) =\left( 1\right) +\left( 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 43;
                                                                                                                                14.4%; S llarity 100.0%; Conservative 0;
                                                                                                                                                                                                                                                                                                                BP; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lemieux B,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /replace= "g"
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                                                                                                                                                                                                                                                                                                                A; 8 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA;
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                                                                                                                                    Mismatches
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RESULT 27 AAX52184/c ID AAX52

AAX52184 standard; DNA; 50 BP

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AAT25074/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       XX
                                                            Query Match
Best Local S
Matches 13
                                                                                                                                                                                                                                                                                          A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in AAR19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost
                                                                                                                                                                                                               all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and proches decimal force).
                                                                                                                                                                           determined (esp. using primers and probes derived sequences) as a means of diagnosing abnormal cell recognising different cell types.
                                                                                                                                               Sequence 50 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
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                                                              Local Similarity nes 13; Conserv
43 TATTTCAAAGTTT
                              12 tatttcaaagttt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene signature
                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 1763; 2245pp; Japanese
                                                               Conservative
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                                                                                                                                               26 A; 3 C; 3 G; 18 T;
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                                                                           14.48;
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                                                                           Score 13;
Pred. No.
                                                               Mismatches
                                                                                                                                               0 other;
                                                                           DB 16; 1
. 2.7e+03;
                                                                                          Length 50;
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                                                                                                                                                                                               for
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                                                                                                                                                                             AAX52048
                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC construct a synthetic DNA plasmid sequence synlux4, to demonstrate the CC construct a synthetic DNA plasmid sequence synlux4, to demonstrate the CC method of the invention. Within the synlux4 sequence are included the CC method of the invention. Within the synlux4 sequence are included the CC sequences of lux A, lux B, the A and B components of the Vibrio fisheril CL luciferase sequence, positions of pUC19 including the origin of CC replication and replication stability sequences, and the promoter and CC coding sequence for tn9 kanamycin/neomycin phosphotransferase. The CC specification describes a method for the synthesis of replication CC competent double-stranded polynucleotides. The method comprises CC generating a first set of oligonucleotides. The method comprises CC strand and a second set corresponding to the minus strand and CC annealing. The method can be used for preparing polynucleotides CC encoding sequences involved in a blochemical pathway. In particular, CC they can be used to produce polynucleotides encoding enzymes.

CC e.g. hexpkinase, phosphohexose isomerase, phosphofructokinase-1, contains the place of the produce polynucleotides contains the place of aldolase, triose-phosphate isomerase, phosphofructokinase-1.
                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 13; Conserv
DNA plasmid; lux A; lux B; Vibrio fisherii; luciferase; tn9 kanamycin/neomycin phosphotransferase; DNA synthesis;
                                                   Synthetic plasmid synlux4 construction oligonucleotide F28
                                                                                          18-JUN-1999
                                                                                                                                                            AAX52048 standard; DNA; 50
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                               dehydrogenase, phosphoglycerate kinase, phosphoglycerate mutase, enolase or pyruvate kinase. They can also be used for the prepa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aldolase, triose-phosphate isomerase, glyceraldehyde-3-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4; Fig 5F; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthesis of replication competent double-stranded polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-244029/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Evans GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TEXA ) UNIV TEXAS SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA plasmid; lux A; lux B; Vibrio fisherii; luciferase; promoter; tn9 kanamycin/neomycin phosphotransferase; DNA synthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic plasmid synlux4 construction oligonucleotide R68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-JUN-1999
                                                                                                                                                                                                                                                                     54 tattgttggagca
                                                                                                                                                                                                                                                   44 TATTGTTGGAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                             viral particles, artificial genomes
                                                                                                                                                                                                                                                                                                                                                                                                              50
                                                                                                                                                                                                                                                                                                                                                                                                              ВP;
                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             competent double-stranded polynucleotide; ss.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             and artificial genetic
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2.7e+03;
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                  promoter;
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RESULT 29
AAX70046/c
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Best Local Similarity
Matches 13; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coding sequence for the kanamycin/neomycin phosphotransferase. The specification describes a method for the synthesis of replication competent double-stranded polynucleotides. The method comprises generating a first set of oligonucleotides corresponding to the plus strand and a second set corresponding to the minus strand and annealing. The method can be used for preparing polynucleotides encoding sequences involved in a biochemical pathway. In particular, they can be used to produce polynucleotides encoding enzymes, e.g. hexokinase, phosphohexose isomerase, phosphofructokinase-1, aldolase, triose-phosphate isomerase, glyceraldehyde-3-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dehydrogenase, phosphoglycerate kinase, phosphoglycerate mutase, enclase or pyruvate kinase. They can also be used for the prepar of viral particles, artificial genomes and artificial genetic sy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAX52021-212 represent oligonculeotide primers that were used to construct a synthetic DNA plasmid sequence synlux4, to demonstrate the method of the invention. Within the synlux4 sequence are included the sequences of lux A, lux B, the A and B components of the Vibrio fisherii luciferase sequence, positions of pUC19 including the origin of replication and replication stability sequences, and the promoter and replication stability sequences.
                                                                                                                                                                                            28-JUL-1999
                                                                                                                                                                                                                             AAX70046;
                                                                                                                                                                                                                                                          AAX70046 standard; RNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 50
                                                                         Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage; tumour anglogenesis; psoriasis; rheumatoid arthritis; ocular disease; fms-like tyrosine kinase 1; kinase insert domain containing receptor;
                                                                                                                                                            Human fltl VEGF receptor hammerhead ribozyme substrate #1341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-244029/20
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                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthesis of replication competent double-stranded polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TEXA ) UNIV TEXAS SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 replication competent double-stranded polynucleotide; ss.
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ω
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                                                                                                                                                                                                                                                                                                                                        tattgttggagca
                                                             liver kinase 1; ss.
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                                                                                                                                                                                           (first entry)
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100.0%;
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Pred. No.
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2.7e+03;
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W09715662-A2

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TE PARKET NEW YEARS OF THE PAR
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AAX70047/c
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes nucleic acid molecules which modulate the synthesis, expression and/or stability of a mRNA encoding 1 or more receptors of vascular endothelial growth factor (VEGF). A patient (preferably human) having a condition associated with the level of the fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be treated by administering the nucleic acid molecule or the expression vector to the patient. AAX67275 to AAX75752 represent specific examples of nucleic acid molecules from the present invention.
(CHIR ) CHIRON CORP.

(RIBO-) RIBOZYME PHARM INC
                                                                                    11-JAN-1996;
26-OCT-1995;
                                                                                                                                                                                                                                    01-MAY-1997.
                                                                                                                                                                                                                                                                                                 WO9715662-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                  flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
fms-like tyrosine kinase i; kinase insert domain containing receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human flt1 VEGF receptor hammerhead ribozyme substrate #1342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAX70047 standard; RNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid molecule modulating VEGF receptor(s) gene expression mRNA stability - useful for treating e.g. tumour angiogenesis, psoriasis, rheumatoid arthritis, etc., in a human patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1997
                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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26-OCT-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                foetal liver
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(RIBO-) RIBOZYME PHARM INC
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llarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP; 8 A; 1 C; 4 G; 4 U; 0 other;
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                                                                                    96US-0584040.
95US-0005974.
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95US-0005974
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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8.3e+03;
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Best Local S
Matches 12
                                                                                                                                                                                                                                                                                                                                                                    Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic; ophthalmologic; antinflammatory; antiarthritic; antipsoriatic; ARMD; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes nucleic acid molecules which modulate the synthesis, expression and/or stability of a mRNA encoding 1 or more receptors of vascular endothelial growth factor (VBGF). A patient (preferably human) having a condition associated with the level of the fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing receptor (KDR) and/or foetal liver kinase 1 (flt-1) (e.g. tumour angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be treated by administering the nucleic acid molecule or the expression vector to the patient. ANX67275 to ANX75725 represent specific examples of nucleic acid molecules from the present invention.
           Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an angiogenic factors \,\cdot\,
                                                                                                                                                                                                                                                                                                                                      myopic degeneration; psoriasis; verruca vulgaris; angiofibroma; tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid molecule modulating VEGF receptor(s) gene expression mRNA stability - useful for treating e.g. tumour angiogenesis, psoriasis, rheumatoid arthritis, etc., in a human patient
                                                              WPI; 1999-591315/50.
                                                                                                                                                              27-MAR-1998;
                                                                                                                                                                                             24-MAR-1999;
                                                                                                                                                                                                                                                            WO9950403-A2
                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                       Kippel-Trenaunay-Weber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Integrin alpha 6 subunit substrate sequence SEQ ID NO:4679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA21453 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17 BP; 8 A; 1 C; 3 G; 5 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escobedo J, McSwiggen
                                                                                                                            (RIBO-) RIBOZYME PHARM INC
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                                                                                              Roberts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ilarity 100.0%;
Conservative (
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                                                                                              Jarvis
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                                                                                                                                                                                                                                                                                                                        Osler-Weber-Rendu syndrome;
                                                                                              Coeshott
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        corresponding target sequences; AAA118385 and AAA19087 to AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086 cand AAA19155 to AAA19222 represent their corresponding target sequences; AAA19223 to AAA23361 and AAA21591 to AAA21595 represent ribozyme compared to AAA21595 to AAA21596 and AAA21596 to AAA21688 represent their corresponding target sequences; AAA21688 to AAA21888 represent their corresponding target sequences; AAA21688 to AAA2188 represent their corresponding target sequences; AAA21688 to AAA23475 and AAA2363 to AAA23472 represent ribozyme sequence for integrin subunit beta 3, and AAA23476 to AAA2362, AAA23343 to AAA23472 represent their corresponding target sequences. The ribozymes of the invention are used for modulating the synthesis, expression and/or stability of an mRNA encoding angiogenic factor, especially ARNV, contention are used for modulating the synthesis, expression and/or stability of an mRNA encoding angiogenic factor, especially ARNV, contention are degeneration (ARND), inflammation, and arthritis, as well as neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris, angiotibroms of tuberous sclerosis, pott-wisher-pendu sendrome variations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                    Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic; ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes enzymatic nucleic acid molecules with RNA cleaving activity, which specifically cleave RNA encoded by an aryl hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3 gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT, and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
Pavco PA,
                                       (RIBO-) RIBOZYME PHARM INC.
                                                                               27-MAR-1998;
                                                                                                                      24-MAR-1999;
                                                                                                                                                                                                   WO9950403-A2
                                                                                                                                                                                                                                           Homo
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                                                                                                                                                                                                                                                                                               myopic degeneration; psoriasis; verruca vulgaris; angiofibroma; tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Integrin alpha 6 subunit substrate sequence SEQ ID NO:4680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4
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Roberts E,
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Jarvis T,
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Pred. No. 8.3e+03;
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Coeshott C,
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McSwiggen JA;
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CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3 cgene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to CC AAA17167 and AAA17561 to AAA17627 represent ribozyme sequences for ARNT, CC and AAA17168 to AAA17560 and AAA17633 to AAA17684 represent their CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to CC AAA19154 represent ribozyme sequences for Tie-2, and AAA19087 to CC AAA19124 represent ribozyme sequences for Tie-2, and AAA19087 to CC and AAA19155 to AAA19222 represent their corresponding target sequences; CC AAA1923 to AAA2361 and AAA21501 to AAA21505 represent ribozyme sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and CAAA21509 to AAA21688 represent their corresponding target sequences; CC AAA21689 to AAA21688 represent their corresponding target sequences; CC AAA21689 to AAA21675 and AAA23363 to AAA23142 represent ribozyme sequence of the invention are used for modulating the synthesis, expression and/or CC constitute of an mRNA encoding angiogenic factor, especially ARNT, CC integrin subunit beta 3, integrin subunit alpha-6, or Tie-2. They are cespecially used to treat cancer, diabetic retinopathy, age related CC macular degeneration (ARMD), inflammation, and arthritis, as well as consistent of tuberous sclerosis, pott-wine stains, Sturge Weber Stundforme. Cistant subarrame of tuberous sclerosis, pott-wine stains, sturge Weber Stundforme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel ribozymes for modulating the synthesis, exprestability of an mRNA encoding an angiogenic factors
Sequence
                                                 syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome, and other syndromes and diseases related to the levels of ARNT, Tie-2, integrin subunit alpha-6, or integrin subunit beta-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention describes enzymatic nucleic acid molecules with cleaving activity, which specifically cleave RNA encoded by an aryl
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BP;
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                                                                                                                   myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
tuberous solerosis; pot-wine stain; Sturge Weber syndrome;
Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss
                                                                                                                                                         ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma;
                                                                                                                                                                                          Human: aryl hydrocarbon nuclear transport; ARNT; TIE-2; anglogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; hammerhead ribozyme; anglogenic factor; cytostatic; antidiabetic; ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
                                                                                                                                                                                                                                                                                                      19-JUN-2000
24-MAR-1999;
                            07-0CT-1999
                                                          WO9950403-A2
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                                                                                      Homo sapiens
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99WO-US06507.
                                                                                                                                                                                                                                                                    subunit substrate sequence SEQ ID NO:4681.
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Pred. No. 8.3e+03;
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Best Local S
Matches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3 gene, an integrin alpha 6 subunit gene, or a Tie 2 gene. AAA16775 to AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT, and AAA17168 to AAA17502 and AAA17623 to AAA17684 represent their corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to AAA19124 represent ribozyme sequences for Tie-2, and AAA19185 to AAA19022 represent their corresponding target sequences; AAA19223 to AAA19223 represent their corresponding target sequences; AAA19223 to AAA20361 and AAA21501 to AAA21505 represent ribozyme sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and AAA21506 to AAA21688 represent their corresponding target sequences; AAA21506 to AAA21688 represent their corresponding target sequences; AAA21506 to AAA21507 and AAA23263 to AAA23342 represent ribozyme sequence integrin subunit beta 3, and AAA23476 to AAA23362, AAA23343 to
                11-APR-2000; 2000WO-US09721.
                                                                                            WO200061729-A2
                                                                                                                                                                        Ribozyme; erythropoietin; granulocyte colony stimulating factor; interferon alpha; ss.
                                                                                                                                                                                                                                 Hammerhead ribozyme substrate #1383
                                                                                                                                                                                                                                                                                                                                                      AAF03088 standard; DNA; 17 BP
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                                                       19-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                        (first entry)
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Pred. No.
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8.3e+03;
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Best Local Similarity
~~+~hes 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP). Inhibition of the repressors removes prevents inhibition (and consequently increases expression of) genes involved in the production of crythropoietin, granulocyte colony stimulating factor
                         Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoletin -
Claim 37; Page 87; 164pp; English.
                                                                                WPI; 2000-647423/62.
                                                                                                                                      (RIBO-) RIBOZYME PHARM INC
                                                                                                                                                                                         11-APR-2000; 2000WO-US09721
                                                                                                                                                                                                                     19-OCT-2000
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                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                   Ribozyme; erythropoietin; granulocyte colony stimulating factor; interferon alpha; ss.
                                                                                                                                                                                                                                                                                                                                           Hammerhead ribozyme substrate #1384.
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                                                                                                                                                                                                                                                                                                                                                                                                                          AAF03089 standard; DNA; 17 BP
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ilarity 100.0%;
Conservative
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                                                                                                        McSwiggen
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. 8.3e+03;
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The present invention relates to enzymatic and antisense nucleic molecules that act as inhibitors of the expression of repressor gencoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA

genes

acid

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RESULT 36
AAF03090/c
ID AAF030
XX AAF030
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Best Local
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                                                                                                                                                                                                                                                                                                                                    The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP). Inhibition of the repressors removes prevents inhibition (and consequently increases expression of) genes involved in the production of erythropoietin, granulocyte colony stimulating factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin -
                                                                                                                                                                                                                                                                                                                the production of erythropoletin, granulocyte protein and interferon alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 37; Page 87; 164pp;
                                                                                                                                                                                                                                                               Sequence 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-APR-2000; 2000WO-US09721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ribozyme; erythropoietin; granulocyte colony stimulating factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hammerhead ribozyme substrate #1385.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (RIBO-) RIBOZYME PHARM INC.
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                                                         4 aaaaaaattatt 15
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                        AAAAAATTATT
                                                                                                                                 l Similarity
12; Conserv
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                                                                                                                                                                                                                                                                  ₽₽;
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                                                                                                                                 Conservative
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Pred. No.
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Pred. No.
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8.3e+03;
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8.3e+03;
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AAF030/C
ID AAF030
XX AAF0310
XX AAF030
XX IO-FEB
XX Ribozy
KW Ribozy
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                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein and
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Best Local Similarity Matches 12; Conserv
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Survivin; inhibitor of apoptosis; IAP; caspase inhibitor; caspase-3; cell cycle regulation; cancer; cytostatic; antisense oligonucleotide;
                                                                     Human survivin DNA antisense oligonucleotide, ISIS 23663
                                                                                                                                                                                                                    AAA08921 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to enzymatic and antisense nucleic molecules that act as inhibitors of the expression of repressor of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 37; Page 87; 164pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ribozyme; erythropoietin; granulocyte colony stimulating factor; interferon alpha; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the production of erythropoietin, granulocyte colony stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (RIBO-) RIBOZYME PHARM INC
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                                                                                                                                                                                                                    DNA;
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Pred. No.
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8.3e+03;
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                                                                                                                                                                                                                                    RESULT
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CC Survivin, an IAP (inhibitor of apoptosis) Caspase inhibitor, and is expressed in the G2/M phase of the cell-cycle in a cell cycle regulated manner and contract with microtubules of the mitotic spindle. Disruption of this interaction results in loss of survivin's anti-apoptotic function and contracted with apoptotic cell death. It is therefore believed that survivin may counteract a default induction of apoptosis in the G2/M phase. It is counteract a default induction of apoptosis in the G2/M phase. It is counteract a default induction of apoptosis in the G2/M phase. It is counteract a default induction of apoptosis in the G2/M phase. It is counteract a default induction of survivin in cancer may consider this apoptotic check point, allowing undesired survival and consorted in cancer cells. Antisense oligonucleotides (ASO's) may be used to down regulate endogenous survivin and to increase caspase-3-dependent cancer cells in the G2/M phase.
                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 12
               Synthetic
                                         FIV; feline immunodeficiency virus; primer; env; cat; petalum amplification; polymerase chain reaction; PCR; vaccine; ss.,
                                                                                               Env gene 5'
                                                                                                                                 21-JUL-1994
                                                                                                                                                                                                   AAQ62806 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18 BP; 1 A; 3 C; 3 G; 11 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This is an antisense oligonucleotide targeted to the coding sequence, nucleotide 393, of human survivin DNA (see AAA08903). AAA08910-49 were analyzed for effect on survivin mRNA levels by quantitative real-time
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Page 66; 73pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antisense molecules targeted to Survivin, useful for inducing apoptosis in cancer cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bennett CF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-SEP-1998;
05-APR-1999;
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modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200018781-A1
                                                                                                                                                                                                                                    39
                                                                                                                                                                                                                                                                                                    51 tcttattgttgg 62
                                                                                                                                                                                                                                                                                      Н
                                                                                                                                                                                                                                                                                                                                                      l Similarity
12; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in cells in the G2/M phase.
                                                                                                 primer.
                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ackermann EJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0163162
99US-0286407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US22076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers 1..18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "phosphorothioate backbone"
                                                                                                                                                                                                                                                                                     12
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; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                   DB 21; 1
. 8.3e+03;
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                                                                env; cat; petaluma;
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                                                                                                                                                                                                                                                                                                                                                                                    Length 18;
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RESULT 40
AAZ69625/c
ID AAZ696
XX
AC AAZ696
XX
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Best Local S
Matches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          derived DNA, obtained from a FIV-infected cat as source of FIV proviral DNA. The primers used are given in AAQ62805-( and AAQ62808-09 and were derived from the nucleotide sequence of the petaluma strain of FIV.
       Novel biallelic markers used to construct a high density disequilibrium map of the human genome \, -
                                                                                                                                                                                                                                                         Human genome; biallelic marker; high density disequilibrium map; genomic map; haplotype; phenotype; polymorphic base; genotyping; haplotyping; hybridisation; identification; characterisation; amplification; single nucleotide polymorphism; SNP; PCR primer;
                                                                                                                21-APR-1998;
23-NOV-1998;
                                                                                                                                                                                                                                                                                                                 Human biallelic marker upstream amplification primer SEQ ID NO:3981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic feline immunodeficiency virus (FIV) polypeptide use in vaccines used to combat {\tt FIV}
                                            WPI; 2000-013267/01
                                                                  Cohen D,
                                                                                         (GEST ) GENSET
                                                                                                                                                                           28-OCT-1999
                                                                                                                                                                                                 WO9954500-A2
                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                         10-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                 AAZ69625;
                                                                                                                                                                                                                                                                                                                                                                                      AAZ69625 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The FIV env gene was amplified by PCR using bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 21; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1994-048871/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Osterhaus ADME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-JUL-1992;
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                                                                  Blumenfeld
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.3%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP; 9 A; 3 C;
                                                                                                                98US-0082614
98US-0109732
                                                                                                                                                    99WO-IB00822
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                                                                  ĭ
                                                                   Chumakov
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                                                                                                                                                                                                                                                                                                                                                                                        ВP
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ore 12; DB 15;
red. No. 8.3e+03;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Siebelink CHJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in AAQ62805-06
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Claim, 8; Page 1080;

2745pp;

English.

present

treatment effects from

The SEQ ID NOS 2852, 2913,

, are not actually given a sequence present invention.

AAZ65654 to AAZ69578 represent human biallelic markers from the present invention, which contain a polymorphic base at position 24 of their nucleotide sequences. AAZ69579 to AAZ77440 represent amplification primers for the biallelic markers. The biallelic markers of the invention have a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also be useful for the identification of the targets for the development of

pharmaceutical agents and diagnostic methods, as well as the characterisation of the differential efficacious responses to and side

pharmaceutical agents acting on a disease as well

2974, 3035,

in 3096,

the

Sequence Listing

0

3157,

3227,

as

other

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Human genome; biallelic marker; high density disequilibrium map; genomic map; haplotype; phenotype; polymorphic base; genotyping; haplotyping; hybridisation; identification; characterisation; amplification; single nucleotide polymorphism; SNP; PCR primer;
   AAZ65654 to AAZ69578 represent human biallelic markers from the present invention, which contain a polymorphic base at position 24 of their nucleotide sequences. AAZ69579 to AAZ77440 represent amplification primers for the biallelic markers. The biallelic markers of the
                                                                                       Novel biallelic markers used
                                                                                                                                                                           98US-0082614
98US-0109732
                                                                                                                                                                                                          99WO-IB00822
                                                                                                                                 Chumakov
                                                       English.
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                                                                                       construct
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see

also

AAQ05904-11

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RESULT 49
AAQ05907
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99999999999999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                 The chemically modified sequences are opposed to the HIV-1 transactivator region, leader sequences (nt 21-53, 74-161, 20 or exon 2 or 3 of the tat gene (nt 5369-5403, 5421-5548, 5581 7967-8366, 8385-9183). This sequence comprises nt 5493-5512 and gives 85% inhibition of HIV-1 tat translation in vitro at concns. of 5-25 microM.
                                complementary sequences can be used as probes to detect HIV. Chemical modification comprises replacing one or more internt phosphodiester linkages by phosphorothioate or methylphosphona
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAQ05907;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pharmaceutical agents and diagnostic methods, as well as the characterisation of the differential efficacious responses to effects from pharmaceutical agents acting on a disease as well
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention have a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also be useful for the identification of the targets for the development of
                                                                                                                                                                   Claim 3(d); Page 8; 15pp;
                                                                                                                                                                                                     Chemically modified antisense oligo-nucleotide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIV mRNA translation inhibiting antisense oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N.B. The SEQ and 3367, are
                                                                                                                                                                                           translation
                                                                                                                                                                                                                                                     Kretschmer,
                                                                                                                                                                                                                                                                Stropp U,
                                                                                                                                                                                                                                                                                                                 09-MAR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ05907 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                        (FARB ) BAYER
                                                                                                                                                                                                                                                                                                                                        25-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified antisense oligonucleotide; HIV mRNA translation inhibition; HIV-1; transactivator region; leader sequence; tat gene; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treatment
                                                                                                                                                                                                                                                                                                                                                                12-SEP-1990
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12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present invention.
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                                                                                                                                                                                                                                                     Baumgarten
, Kolbl H,
                                                                                                                                                                                           of HIV MRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Α,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2852,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 C;
                                                                                                                                                                                                                                                      Frommer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2913,
                                                                                                                                                                    German.
                                                                                                                                                                                                                                                                Lobberding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 21;
8.3e+03;
                                                                                                                                                                                                                                                                 Springer
                                  or methylphosphonate
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                                                                                                                                                                                                                                                                 Σ,
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                                                                                                                                                                                                     inhibiting
                                                                                                                                                                                                                                                                   Piel
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                                                                                                                  61, 202-279)
, 5583-5617,
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well as other
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DЬ Qy

18

downstream amplification

primer

SEQ ID

NO:9482

BP

73

ccaatgaaagca 84 CCAATGAAAGCA 7

Query Match Best Local

Similarity

13.3%;

Score Score 12; Pred. No.

DB 21; 8.3e+03;

21;

Length 19

Conservative

0

Mismatches

0;

Indels

0;

Gaps

0

Sequence 19 BP; 1 A; 4 C; 5 G;

9 T;

0 other

Matches

SS

Sequence

20

BP; 8 A;

4 C;

3 G;

5 T; 0 other

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ΧIJ
                                                RESULT 44
AAV72697/c
                                                                                                                                                      Вb
                                                                                                                                                                                                      QΥ
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AAT80813/c
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Best Local Similarity
Watches 12; Conserv
                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a PCR primer used in the present invention describing novel polypeptides, which can optionally be expressed in NCIMB 40771. The polypeptides, and polynucleotides encoding it, are derived from Staphylococcus aureus. Cells expressing ligands binding the polypeptides can be used to isolated candidate compounds that bind and inhibit the activity of the polypeptides. Such compounds can be used as anti-bacterial compounds. The polypeptides may also be used as immunogens to vaccinate an animal for protection against
                        AAV72697
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20
                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus aureus caused disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New Staphylococcus aureus polynucleotide and polypeptide(s) - for isolating antagonist of the polypeptide(s) useful as anti-bacterials (x,y) = (x,y) + (y,y) + (y,y)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-435166/40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus Gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-FEB-1997;
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                                                                                                                                                                                                                                                      Local Similarity nes 12; Conserv
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|||||||||||||
| 2 caatgaaagcaa 13
                                                                                                                                                                                                      39 gttttcatgttt 50
                                                                                                                                                      GTTTTCATGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disease;
                        standard;
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Conservative 0
                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                       BP; 11 A; 4 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aureus WCUH 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96GB-0004045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97WO-GB00524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protection;
                        DNA;
                                                                                                                                                                                                                                                                                 13.3%;
                        20
                                                                                                                                                                                                                                                                                                                                                                                       2 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #22 PCR primer sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         kernel oil concentration. The method comprises: (a) selecting a corn plant from a breeding population using at least one of the genetic markers s1375, s1384, s1394, s1416, s1422, s1432, s1457, s1480, s1476, s1478, s1484, s1500, s1513, s1529, s1544, s1545, s1630, s1633, s1647, s1780, s1750, s1751, s1772, s1774, s1780, s1797, s1813, s1816, s1817, s1836, s1853, s1860, s1870, s1921, s1922, s1925, s1931, s1933, s1939, s1946, s1949, s2054, s2055, s2057, s2058, s2097, s2122, s2125, s1939, s1946, s1949, s2054, s2055, s2057, s2058, s2097, s2122, s2125, s1939, s1946, s1949, s2054, s2055, s2057, s2058, s2097, s2122, s2125, s21930, s2156, and s2175; and (b) crossing the selected plant with a second plant and obtaining progeny with increased kernel oil concentration. Also described are: (1) a method for identifying corn plants or lines for use a parents to create a breeding population, for the content of the second plants or lines for use a parents to create a breeding population of the second plants or lines for use a parents to create a breeding population.
                                                                                                                                                                                                                                                                                                                                                                                                                        comprising: (a) genotyping corn plants or lines with one or more of the above genetic markers; and (b) identifying plants or lines which are predicted to produce transgressive segregants for kernel oil concentration; and (2) trait loci controlling kernel oil concentration mapped by the above genetic markers, with the exception of s1480.

AAV72694 to AAV72797 represent PCR primers which are used to amplify the genetic markers for use in the method of the invention.
                                      13-SEP-1999
                                                                                                                AAX92327 standard; DNA;
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PCR primer used to amplify an ORF of Chlamydia pneumoniae.

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Search completed: January 24, 2002, 03:28:21 Job time: 3673 sec
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Best Local Similarity
                                                                                                                                                                                                                                 AAX391991-X97517 represent PCR primers used to amplify open reading frames and other nucleic acid sequences from the genome of Chlamydia pneumoniae (see AAX91990). C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-AAY35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope; PCR primer; ss.
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h Simi 16;	HIT 1 8-816-977-12 8-816-977-12 8-816-977-12 guence 12, Applicate tent No. 6080400 ENERAL INFORMATION: APPLICANT: Willia APPLICANT: Byrne, APPLICANT: Byrne, APPLICANT: Byrne, APPLICANT: Byrne, APPLICANT: COUNTRY OF INVENTION NUMBER OF SEQUENCE CORRESPONDENCE ADDERSSEE: Medl STREET: 220 Medl STREET: 220 Medl STREET: 220 Medl STREET: 220 Medl STREET: READABLE MEDIUM TYPE: FILE COMPUTER: IBM FOPERATING SYSTEM SOFTWARE: PATEN NUMBER SOFTWARE: PATEN SOFTWARE: PATEN SOFTWARE: APPLICATION NUMBER SOFTWARE: NAME: MACKNIGHT REGISTRATION NUMBER FILING DATE: 13 CLASSIFICATION PREFERENCE/DOCKET TELEPHONE: (415) SOUIENCE CHARACTER LENGTH: 29 base TYPE: DUCLORS: STRANDEDNESS: STRA		
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Patent No. 5525495
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                                                                      TITLE OF INVENTION:
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NUMBER OF SEQUENCES:
                                                                                                                      APPLICANT: KEENE, JACK D.
APPLICANT: KING, PETER H.
APPLICANT: LEVINE, TODD
TITLE OF INVENTION: METHO
                                                        CORRESPONDENCE ADDRESS
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NAME: KIT, Gordon
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: NORIEGA, Fernando APPLICANT: LEVINE, Myron M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                              189 aaaataattatttta 204
        ADDRESSEE:
ADDRESSEE:
STREET: 17
                                                                                                                                                                                                                                                                                                              14 AAAATAATTATTTTA 29
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FILING DATE: 9-APR-
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 2100 Pennsylva
CITY: Washington, D.C.
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 30,764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                          INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          l Similarity 100.0%;
16; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
                                                                                                                                                                                                                           Application US/08120827
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3: P.C.
1755 Jefferson Davis Highway, Fourth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                     OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
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                                                                                         RECOGNITION, BINDING AND EXPRESSION OF RIBONUCLEIC ACIDS INVOLVED IN CELL GROWTH, NEOPLASIA AND IMMUNOREGULATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GUA MUTANTS OF SHIGELLA AND VACCINES CONTAINING 18
                                                                                                                       METHODS AND COMPOSITIONS USEFUL IN THE
                                                                         101
                                                                                                                                                                                                                                                                                                                                                                                                           4.9%;
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                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 36;
3e+02;
hes 0; Indels
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)413-3000
TELEFAX: (703)413-2220
TELETX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
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EILING DATE: 07-JUN-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/120,82
EILING DATE: 15-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5773246man F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: KEENE, JACK D. APPLICANT: KING, PETER H. APPLICANT: LEVINE, TODD TITLE OF INVENTION: METHODS TITLE OF INVENTION: RECOGNITITLE OF INVENTION: INVOLVENTION:
                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/08/120,827
FILING DATE: 15-SEP-1993
                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, McCLELLAND,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5525495man F.
REGISTRATION NUMBER: 24,618
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                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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Local Similarity 33.3%;
nes 5; Conservation
                                                                                                                    APPLICATION NUMBER: US/08/478,675 FILING DATE: 07-JUN-1996
                                                                                                                                                                                                                                                                                                                     CITY: Arlington
STATE: Virginia
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TOPOLOGY: un
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CLASSIFICATION:
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o. 5773246
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                                                                                                                                                                                                                                                                                                                                                                                                                                         101
                                                              us 08/120,827
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Pred. No. 7.9e+0
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                   APPLICATE: 1992141-
EILING DATE: 1992141-
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/826,934
APPLICATION NUMBER: 21-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (703)413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fablan, Gary R.
                                                                                                                              TELEFAX: (415) 859-3880 ENFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Jayasena, Sumedha D.
APPLICANT: Johnston, Brian H.
TITLE OF INVENTION: Triple Helix Formation at
TITLE OF INVENTION: (PUNPYN)-(PUNPYN) Tracts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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ADDRESSEE: SRI International
STREET: 333 Ravenswood Avenue
                 HYPOTHETICAL: NO ORIGINAL SOURCE:
                                               MOLECULE TYPE:
                                                                                                                                                                            REFERENCE/DOCKET NUMBER: P-3141
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 859-4550
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                                                                                               TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 333 Raver
CITY: Menlo Park
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                                                                    TOPOLOGY: 1i
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INDIVIDUAL ISOLATE: OLIGONUCLEOTIDE III, FIGURE
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                                                 DNA (genomic)
                                                                                  single
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                                                                                                                                                                                                                                                                                              US 07/808,452
                                                                                                                                                                                                                                33,875
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US-08-852-299-29/c
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                                                                                                           Sequence 29, Application US/08852299 Patent No. 6010897
                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
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Best Local Similarity
Matches 15; Conserv
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                                                                                             GENERAL INFORMATION:
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CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                APPLICANT:
                                                 APPLICANT:
                                                              APPLICANT:
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LENGTH: 32 base pairs
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    TITLE OF INVENTION:
                   APPLICANT:
                                                                                                                                                                                                                     154 aaaggaaaatataaa 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                        DLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA from
DESCRIPTION: oligonucleotide synthesis"
                                                                                                                                                                                                     30 AAAGGAAAATATAAA
                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U
ZIP: 10020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/08256261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Fish & Neave
1251 Avenue of the Americas
                            Schlott, Bernhard
Albrecht, Sybille
G hrs, Karl-Heinz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schlott, Bernhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Behnke, Detlef
Hartmann, Manfred
/ENTION: Expression of signal-peptide-free
                                                                             Behnke, Detlef
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G hrs, Karl-Heinz
                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Albrecht, Sybille
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                     single
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100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               staphylokinases
                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Expression of signal-peptide-free
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Manfred
                                                                                                                                                                                                                                                                                              4.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/08/256,261
                                                                                                                                                                                                                                                            Score 15; DB 1; Le
; .Pred. No. 7.7e+02;
.: .matches 0;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 5; L 7.8e+02;
                                                                                                                                                                                                                                                                                           Length 32;
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                                                                                                                                          ; OTHER INFORMATION: Antisense Oligonucleotide US-09-205-204-20
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Best Local Similarity
""+ hes 15; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                               us-09-205-204-20/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-852-299-29
                                                                                                                                                                                                                    TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR INHIBITOR OF APOPTOSIS-1 EXPRESS FILE REFERENCE: RTS-0020
CURRENT APPLICATION NUMBER: US/09/205,204
CURRENT FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 20
LENGTH: 18
                                                             Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20, Application US/09205204
Patent No. 5958772
                                                                                                                                                                                                                                                                                                                               APPLICANT: C. Frank Bennett
APPLICANT: Elizabeth J. Ackermann
APPLICANT: Lex M. Cowsert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                        FEATURE:
                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
DESCRIPTION:
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APPLICATION NUMBER: 08/256,261
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160 aaatataaataaaa 173
18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 17-MAY CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York
STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.6%; Score 15; ilarity 100.0%; Pred. No. Conservative 0; Mismatc
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                                                              Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    other nucleic acid
/desc = "synthetic DNA from
oligonucleotide synthesis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     staphylokinases
                                                                           4.3%; Score 14; DB 2; L
100.0%; Pred. No. 2.1e+03;
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                                                              Mismatches
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                                                                                          Length 18
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                                                             Gaps
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                                                                                                                                                                                                                                                                                                                   RESULT 10
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Matches
                                                                                                                                                                                                                               Sequence 31, Application US/08629001A
Patent No. 5858661
GENERAL INFORMATION:
APPLICANT: Shiloh, Yosef
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 397-833
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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APPLICANT:
ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: OF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 13-MAR-199
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                   NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                 189 aaaataattatttt 202
                                                                                   CITY: Farmington Hills STATE: Michigan COUNTRY: US
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                  22 AAAATAATTATTTT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29 base pairs
                                                                                                                                    E: Kohn & Associates
30500 No. 5858661thwestern Hwy
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Pugh, Charles S.G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (415) 397-8338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-MAR-1997
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                                                                                                                                                                                                    GENOMIC
                                                                                                                                                                                                    ATAXIA-TELANGIECTASIA GENE AND ITS GENOMIC ORGANIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Verotoxin-Induced Disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                               4.3%; Score 14;
100.0%; Pred. No.
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. 2e+03;
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US-08-629-600-16/c
Sequence 16, Application US/08629600
Patent No. 5783196
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Shiloh, Yosef
TITLE OF INVENTION: MUTATE
TITLE OF INVENTION: SCREEN
FILE REFERENCE: 229000033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-642-274D-110
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SEQ ID NO 110
LENGTH: 30
TYPE: DNA
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Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/08/642,274D CURRENT FILING DATE: 1996-05-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (810) 539-5055 INFORMATION FOR SEQ ID NO: 31:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: 2290
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810) 539-5050
NERAL INFORMATE.

APPLICANT: NORIEGA, FETHAR.

APPLICANT: LEVINE, MYTON M.

TITLE OF INVENTION: AUD VACCINES CONTAINING THE SAME

"TTTLE OF INVENTION: AUD VACCINES CONTAINING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence:intronic OTHER INFORMATION: sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                         196 ttatttttatttta 209
                                                                                                                                                                                                                                                        14 ttatttttatttta 27
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH:
                                                                                                                                                                                                                                                                         14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.3%; S ilarity 100.0%; Conservative 0;
                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MUTATED FORMS OF THE ATAXIA-TELANGIECTASIA GENE AND METHOD TO SCREEN FOR A PARTIAL A-T PHENOTYPE
                                                                                                                                                                                                                                                                                                                    4.3%; Jr
100.0%; Pr
0;
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                                                                                                                                                                                                                                                                                                                                        Score 14; DB 4;
Pred. No. 2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 14; DB 2; Length 30; Pred. No. 2e+03;
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                                                                                                                                                                                                                                                                                                                                                          Length 30;
                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (202) 293-7860
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/0
FILING DATE: 9-APR-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: KIT, GORDON
                                          SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 30,764
REFERNCE/DOCKET NUMBER: ATTELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
                                                                                                                                                                                                                                                                        APPLICANT: COLMAN, PETER M.
TITLE OF INVENTION: TARGET BINDING POLYPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
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                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189 aaaataattatttt 202
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CITY: Washington,
                                                                                                                                                                           CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 AAAATAATTATTT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                           APPLICATION NUMBER:
                                                                                                                                            ZIP:
                                                                                                                                                          COUNTRY:
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                                                                                                                                            20007-5109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/08403853
                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                    IRVING, Robert A. ATWELL, John L. MALBY, Robyn L.
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                                                                                                                                                                                                                                                                                                                                                                         KORRT, Alex A.
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30-MAY-1995
V: 435
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100.0%;
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                            US/08/403,853
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Pred. No.
                                                                                                                                                                                                         Suite 500
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FILING DATE: 24-SEP-1993 PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

WO PCT/AU93/00491

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Best Local S
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                                              CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/749,805
FILING DATE: 16-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/006,831
FILING DATE: 16-NOV-1995
ATTORNEY,AGENT INFORMATION:
NAME: DOYLE LEARY Ph.D., KATHRYN
REGISTRATION NUMBER: 36,317
REFERENCE,DOCKET NUMBER: 9596-2302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: AU PL 497:
ETLING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 1678/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: BOEKE, JEF D.
APPLICANT: MORAN, JOHN V.
APPLICANT: DOMBROSKI, BETH A.
                  TELECOMMUNICATION INFORMATION: TELEPHONE: 215-567-2020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE TITLE OF INVENTION: MAMMALIAN RETROTRANSPOSONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/0 FILING DATE: 28-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: PHILADELPHIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 37 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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6150160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: PANITCH SCHWARZE JACOBS & NADEL, P.C. ONE COMMERCE SQUARE, 2005 MARKET STREET,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       U.S.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KAZAZIAN JR., HAIG H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative (
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25-SEP-1992
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                                                       9596-2302
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В
; OTHER INFORMATION: Synthetic Sequence US-09-288-461-79
                                                                                                                                                                                                                                                                                                          US-09-288-461-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-686-968C-13
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                                                                                 CURRENT APPLICATION NUMBER: US/09/288,461
CURRENT FILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 79
LENGTH: 20
                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Karras, James G.
                                                                                                                                                                                                                                                                     Sequence 79, Application US/09288461
Patent No. 6159694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 18
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Best Local Similarity
Matches 13; Conserv
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Patent No. 6221361
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Matches 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/08/686,968C CURRENT FILING DATE: 1996-07-25 NUMBER OF SEQ ID NOS: 231
                                                                                                                                                                                                   TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3 TITLE OF INVENTION: Expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cochran, Mark D.
APPLICANT: Junker, David E.
TITLE OF INVENTION: Recombinant Swinepox Virus
FILE REFERENCE: 39119-H/JML
                                                                                                                                                                                       FILE REFERENCE: ISPH-0338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                 ORGANISM: Artificial Sequence FEATURE:
                                                                   TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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Pred. No.
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Query Match

4.0%;

Score 13;

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Length 20;

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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Oligonucleotide
US-08-691-045-61
                                                                                                                                                                                                  US-08-672-215-1/c
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                                                                                                                                                              Sequence 1, Application US/08672215
Patent No. 6020121
                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (414) 277-5000
TELEFAX: (414) 271-3552
INFORMATION FOR SEQ ID NO: 61
                                                                            APPLICANT: Ving Bao, Amy Boggs, Pamela R. Contag, APPLICANT: Nancy A. Federspiel, Alan Herbert, APPLICANT: Scott J. Hecker, Francois Malouin TITLE OF INVENTION: INHIBITORS OF REGULATORY PATHWAYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Henrickson, Kelly J.
APPLICANT: Fan, Jiang (n.m.i.)
TITLE OF INVENTION: VIRUS ASSAY METHOD
                                              NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Baker, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 651
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173 atttagataaaag 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Polocia
                                                                                                                                                                                                                                                                      17 TATATGATAAGTA 5
                                                                                                                                                                                                                                                                                                   94 tatatgataagta 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Milwaukee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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53202-4497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 base pairs
E: Lyon & Lyon 633 West Fifth Street Suite 4700
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                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6
Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
            COMPUTER READABLE FORM:
MEDIUM TYPE: F1Dppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/120,827
                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                 APPLICANT: KEENE, JACK D. APPLICANT: KING, PETER H. APPLICANT: LEVINE, TODD
                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     294 tgtaatttttatg 306
                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                               STREET: 1755 Jei
CITY: Arlington
STATE: Virginia
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                                                                                                                                            COUNTRY:
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                                                                                                                              22202
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California
                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/08120827
                                                                                                                                                                                               1755 Jefferson Davis Highway, Fourth Floor
                                                                                                                                                                                                                                                                                                                                                                  KEENE,
                                                                                                                                                U.S.A.
                                                                                                                                                                                                                                OBLON,
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METHODS AND COMPOSITIONS USEFUL IN THE RECOGNITION, BINDING AND EXPRESSION OF INVOLVED IN CELL GROWTH, NEOPLASIA AND

RIBONUCLEIC

SPIVAK, MCCLELLAND, MAIER & NEUSTADT

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Query Match
Best Local Similarity
                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: WAIDLITY, RICHARD J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 219/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/004,626
FILING DATE: September 29, 1995
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastsEQ for Windows 2.0
CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: storage
                                                                                                                                                                                           TELEFAX: (21)
TELEFAX: 67-3510
TOTEX: 67-3510
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/
FILING DATE: June 25, 1996
CLASSIFICATION: 514
                                                                                                                     STRANDEDNESS: single
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                                                                                                                                                                                                                             (213) 955-0440
 Conservative
                  4.0%;
100.0%;
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                Score 13;
Pred. No.
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   Mismatches
                                  DB 3;
                  5.1e+03
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ATTORNEY/AGENT INFORMATION:

CLASSIFICATION:

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                                                                                                                                                                 CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/120,827
FILING DATE: 15-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5773246man F.
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (703)413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
SEQUENCE STATEMENT OF PAGE DAILS
                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 28 base pairs
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: LEVINE, TOOD
TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL IN THE
TITLE OF INVENTION: MECOGNITION, BINDING AND EXPRESSION OF RIBONUCLEIC ACIDS
TITLE OF INVENTION: INVOLVED IN CELL GROWTH, NEOPLASIA AND IMMUNOREGULATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                    TELECOMMUNICATION INFORMATION:
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TELEX: 248855 OPAT UR
TELEX: 248855 OPAT UR
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OPERATING SYSTEM:
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CITY: Arlington
STATE: Virginia
                                                                                                 TELEPHONE: (703)413-3000
TELEFAX: (703)413-2220
                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/478,675 FILING DATE: 07-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.
ZIP: 22202
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STRANDEDNESS:
                                                                                                                                                      REFERENCE/DOCKET NUMBER:
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o. 5773246
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: nucleic acid
NDEDNESS: unknown
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               nucleic acid
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(703)413-2220
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KING, PETER H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
                                                                                                                                                                                                                                                                                                                                                             IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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; Pred. No. 5e+0
11; Mismatches
                                                                                                                                                      714-158-0 CIP
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GENERAL INFORMATION:
APPLICANT: Shiloh, Y
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 2290
                                                                                                           RESULT 22
US-08-642-274D-158
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                                                                            Sequence 158, Application US/08642274D Patent No. 6200749
                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS: LENGTH: 30 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown
MOLECULE TYPE: RNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 48334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Farmington Hills
STATE: Michigan
                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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o. 5858661
                                                                                                                                                                                                                                             13;
                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
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30500 No. 5858661thwestern Hwy.
                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (810)
   229000033
                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                 0) 539-5055
) 539-5055
: NO: 79:
              MUTATED FORMS OF THE ATAXIA-TELANGIECTASIA GENE AND METHOD SCREEN FOR A PARTIAL A-T PHENOTYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    539-5050
                                                                                                                                                                                                                                                          100.0%;
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                                                                                                                                                                                                                                                       4.0%; Score 13; DB 2;
100.0%; Pred. No. 4.9e+03
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5.4%; Pred. No.
                                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                                                                                         Length 30;
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; OTHER INFORMATION: Description of Artificial Sequence:intronic; OTHER INFORMATION: sequence US-08-642-274D-158
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Best Local Similarity 100.

Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/08330638D Patent No. 5731425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 588-2405
TELEPAX: (716) 477-4646
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 30
TYPE: DNA
ORGANISM: Artificial Sequence
                                MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                            FILLING DATE: 28 OCT 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA: NONE
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: WORD FOR WIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: POLYPEPTIDE SURFATITLE OF INVENTION: MARKER FOR CELLS NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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                    ORIGINAL SOURCE:
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 [MMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          272 aaaaaaattatttc 284
                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette, 3.5 inch,
MEDIUM TYPE: 1.44 MB storage, (Hewlett Packard)
COMPUTER: HP Vectra
OPERATING SYSTEM: MS-DOS Version 6.0
                                                                                                                                                                                                                                                            NAME: Kiernan, Anne B
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                    STRANDEDNESS: SII
                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 14650-2201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Rochester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Eastman Kodak Company, ADDRESSEE: Patent Legal Staff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 aaaaaattatttc 27
                                                                                                                                        LENGTH:
                                                                                                                    NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                343 State Street
                                                                                                                                          31 BASES
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Chubet, Richard
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                                                                                                                                                                                                                                                                                                                                                                                                    WORD FOR WINDOWS
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                                                    No
                                                                                                                                                                                                                                                                                                                                              UMBER: US/08/330,638D
28 OCT 1994
                                                                     SYNTHETIC OLIGONUCLEOTIDE
                                                                                                        SINGLE
SYNTHETICALLY PREPARED SYNTHETICALLY PREPARED
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RESULT 25
US-08-247-809A-14/c
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                                                                                                                                                                                                       US-08-906-746A-5
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                                                                                                                                Best Local Similarity
Matches 13; Conser
                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/906,746A
FILING DATE: 06-AUG-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                 HYPOTHETICAL:
                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 314-231-5400
                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Stone, Paul A.
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Method of Identifying Cells with TITLE OF INVENTION: Polypeptide Surface Marker NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hopp, Thomas P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                           124 gtgttctcggggg 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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                                                                          GTGTTCTCGGGGG
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                                                                                                                                                                                                                                                                                                                                                  314-231-4342
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                                                                                                                                  Conservative
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Bianca, Darlene W.
                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                             DNA (genomic)
                                                                                                                                                                                                                                                                          single
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Pred. No.
                                                                                                                                               Score 13; DB 2;
Pred. No. 4.9e+
                                                                                                                                  Mismatches
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                                                                                                                                               4.9e+03;
                                                                                                                                                             Length 31;
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                                                                                                                                Indels
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                                                                                                                                Gaps
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APPLICANT: Peter H. Schreier; Klaus Stenzel; Gunter Adam; APPLICANT: Edgar Maiss

INFORMATION:

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                                                                                                                                                                                                                                                                            Sequence 14, Approx No. 5973135
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                                                                                                                                                                                                                                                                   Patent No. 5973135
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: Bayer 9049-KGB
TELECOMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
TELEPAX: (914) 332-1844
                                                    COMPUTER READABLE FORM:
                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                              APPLICANT: Peter H. Schreier; Klaus Stenzel; Gunter Adam; APPLICANT: Edgar Maiss
TITLE OF INVENTION: DEOXYRIBONUCLEIC ACIDS
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: P 43 178 45.6 (Germany)
FILING DATE: May 28, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Kurt G. Briscoe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
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CTTY: Tarrytown
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                                                                                   STATE: New York COUNTRY: U.S.A.
                                                                                                                     STREET: 660 Whi
                                                                                                                                                                                                                                                                                                                                                                                                 24 AGGAAAATATAAA 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette, MEDIUM TYPE: storage
                MEDIUM TYPE: Diskette, 3.50 inch, MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
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COMPUTER:
                                                                                                                                                          ADDRESSEE:
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                                                                                                                                                                                                                                                                                                        Application US/08711728
                                                                                                                                         E: SPRUNG HORN KRAMER & WOODS 660 White Plains Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          660 White Plains Road
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NEC Powermate 1 Plus
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US-08-097-554A-45
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Matches
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 37 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
                                                                                                                                                                          COMPUTE: IBM PC compatible
COMPUTE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
COURTENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,554A
FILING DATE: July 22, 1993
FILING DATE: July 22, 1993
                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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LENGTH: 36 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/247,809 FILING DATE: 23-MAY-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cochran Ph.D., Mark D
APPLICANT: Junker M.S., David E
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: DE 43178456 FILING DATE: 28-MAY-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
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Local Similarity 100.0%; Pred. No.
hes 13; Conservative 0; Mismatc
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                                                                         TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                                                    CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (914) 332-1700
TELEFAX: (914) 332-1844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: Bayer 9049.1-KGB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOFTWARE: WordPerfect 5.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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                                                            422523
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                                                                             (212)664-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                         John P.
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nucleic acid

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; CLONE: 515-85.1
; POSITION IN GENOME:
; MAP POSITION: -23
; UNITS: %G
US-08-097-554A-45
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US-08-484-575A-10
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                                                                                                            US-08-484-575A-10
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Best Local Similarity 100.0%;
Matches 13; Conservative
                                               Query Match
Best Local
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                                Matches
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                                                                                                                                                                                                                                                 TELEFAX: (212)391-0525
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: White Esq, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)278-0450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: LILL
STREET: New York
CITY: New York
TATE: New York
                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/484,575A
FILING DATE: 07-JUN-1995
                                                                                                                         MOLECULE TYPE:
HYPOTHETICAL: I
ANTI-SENSE: NO
                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 37 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESSE: John P. White
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     231 aattgaattgtaa 243
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CLONE: 515-85.1
231 aattgaattgtaa 243
                                                                                                                                                                                TYPE: nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 AATTGAATTGTAA 22
                              Local Similarity
nes 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
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                                                                                                                                                                                                 nucleic acid
                              Conservative 0;
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                                                             4.0%;
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                             Score 13; DB 2;
Pred. No. 4.8e+(
0; Mismatches
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Pred. No. 4.8e+
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                              4.8e+03;
hes 0;
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                                                          Length 37;
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; HYPOTHETICAL:
; ANTI-SENSE: N
US-08-477-459-10
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                                                                                                                                                                                                                                    Sequence 45, Application US/08480640A Patent No. 6033904
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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APPLICANT: Cochran, Mark D.
APPLICANT: Junker, David E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Mark D. CO
TITLE OF INVENTION: I
TITLE OF INVENTION: I
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,459
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White Esq, John P
TELECOMMUNICATION INFORMATION:
                                                                                                                                  TITLE OF INVENTION: RENUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 37 base pairs
TYPE: nucleic acid
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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                                                                    STREET: 1185 ACCITY: New York
STATE: New Yor
                                                   COUNTRY: USA
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                                                                                                                    ADDRESSEE:
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                                     10036
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1185 Avenue of the Americas
                                                                                                 1185 Avenue of the Americas
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(212) 391-0525
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                                                                                                                    John P. White
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                                                                                                                                                                    Recombinant Swinepox Virus
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

US/08/480,640A

OPERATING SYSTEM:

IBM PC compatible SYSTEM: PC-DOS/MS-DOS

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US-08-479-869-10
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US-08-480-640A-45
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Best Local Similarity 100.0%;
Matches 13; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (212) 391-052:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 base pairs
                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cochran Ph.D, Mark D
TITLE OF INVENTION: Recombinant Fowlpox Virus S-FPV-043 and
TITLE OF INVENTION: Uses Thereof
APPLICATION NUMBER: 08/0 FILING DATE: 26-FEB-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
                                              CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POSITION IN GENOME:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: White, John P REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231 aattgaattgtaa 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Swinepox virus
STRAIN: Kasza
INDIVIDUAL ISOLATE: S-SPV-001
                                                                                  FILING DATE:
                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                     CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                    STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: doub
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                      10112
                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                      30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                     John P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NO
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100.0%; Pred. No.
                                                                                                  US/08/479,869
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US-08-295-802-45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 45, Application US/08295802
Patent No. 6127163
GENERAL INFORMATION:
APPLICANT: Cochran Ph.D., Mark D
APPLICANT: Junker M.S., David E
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Best Local Similarity
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TELEX: 422523
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                 TELEFAX: (212)664-0525
TELEX: 422523
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/295,802
                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEFAX: (212)664-0525
IMMEDIATE SOURCE:
CLONE: 515-85.1
                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (212)977-9550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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HYPOTHETICAL: NO
                                                                         ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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                                                                                                       HYPOTHETICAL:
                                                                                                                       MOLECULE TYPE:
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                            ORGANISM: Swinepox
STRAIN: Kasza
INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: Herew
                                                                                                                                         TOPOLOGY:
                                                                                                                                                                  TYPE: nucleic acid
                                                                                                                                                                                                                                                                                             NAME: White,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
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                                                                                                                                                  STRANDEDNESS:
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                                                                                                                                                                                  ENGTH:
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                                                                                                                                                                                    37 base pairs
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30 Rockefeller Plaza
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                                                            Swinepox virus
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100.0%;
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                               S-SPV-001
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US-08-488-237A-45
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US-08-486-414-10
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US-08-295-802-45
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                                                                                                                                                                                                                                                                                                                                                                                                                                  S-08-46, Approx. Sequence 45, Approx. No. 6251403
                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 6251403
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 13; Conserv
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LENGTH: 37
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Best Local Similarity
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CURRENT FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cochran, Mark D.
APPLICANT: Junker, David E.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUSES AND USES THEREOF
FILE REFERENCE: 42771D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Cochran, Mark D. APPLICANT: Junker, David E.
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                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                      APPLICATION NUMBER: US/0 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                      STATE:
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                                                                                                                                                                                                                                                                                     New York
                                                                                                                                                                                                                                                                   New York
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                                                                                                                                                                                                                                                                                                     1185 Avenue of the Americas
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Pred. No.
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Pred. No. 4.8e+03
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APPLICANT: Syntro Corporation, et a
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TOPOLICAL: DNA MOLECULE TYPE: DNA HYPOTHETICAL: NO
                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (212) 391-0525 INFORMATION FOR SEQ ID NO:
                                                                                                                                                               NAME: White ESG, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
TELEPAX: (212)664-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Syntro Corporation, et al.
TITLE OF INVENTION: Recombinant Fowlpox Virus S-FPV-043 and Uses Thereof
NUMBER OF SEQUENCES: 20
                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 37 base pairs
                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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MAP POSITION: ~2
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LENGTH: 37 base pairs
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CLONE: 515-85.1
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HYPOTHETICAL:
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                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                               FILING DATE: 2
CLASSIFICATION:
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CTREET: 30 Rockefeller Plaza
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STRANDEDNESS: double
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                                                                                   nucleic acid
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                                    DNA (genomic)
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100.0%; Pred. No.
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. 4.8e+03;
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TELEX: 422523
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 37 base pairs
TYPE: nucleic acid
                                                                                                                                                                    Sequence 40, Application PC/TUS9600547 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 13; Conserv
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Best Local Similarity 100.0%;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATING SYSTEM: PC-DOS/MS-DOS
                                                                                                   TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: White Esq, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                 CORRESPONDENCE ADDRESS
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CURRENT APPLICATION DATA:
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COUNTRY: U.S.A
                   STATE:
                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US94/02252A
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                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13;
              SSEE: Curtis, Morris & Safford, P.C.
1: 530 Fifth Avenue, 25th Floor
New York
: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: John P. White
30 Rockefeller Plaza
                                                                                                                                  Virogenetics Corporation

VENTION: RECOMBINANT POXVIRUS-HTLV, COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Syntro Corporation, et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               double
                                                                                                 AND USES
                                                                                                                                                                                                                                                                                                                                                        4.0%; Score 13; DB 5; L
100.0%; Pred. No. 4.8e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant Fowlpox Viruses and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20
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                                                                                                                                                                                                                                                                                                                                            0;
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                                                                                                                                                                                                                                                                                                                                                                        Length 37;
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                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 5494807 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 168, Application US/08105483 Patent No. 5494807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (212) 840-07: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PATENCE.
SOFTWARE: PATENCE.
CURRENT APPLICATION NUMBER: PCT/U
APPLICATION NUMBER: PCT/U
APPLICATION 12-JAN-1996
                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,951
FILING DATE: 06-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: PAOLETTI, ENZO
TITLE OF INVENTION: GENEFICALLY ENGINEERED VACCINE
TITLE OF INVENTION: STRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 13-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: cDNA
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                          STREET: 530 F1:
CITY: New York
STATE: NY
               REGISTRATION NUMBER: 25,506 REFERENCE/DOCKET NUMBER: 45
                                                                                                                                                                    APPLICATION NUMBER: US/08/105,483 FILING DATE: 12-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 1
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: C/O William S. Frommer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 454310-2621
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REGISTRATION NUMBER: 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                           10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                  530 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (212) 840-0712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.0%; Score 13; DB 5;
100.0%; Pred. No. 4.7e+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          462
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                 454310-2400
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TELEPHONE:

(212) 840-3333

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LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-709-209-168
                δð
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US-08-709-209-168/c
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                                               Matches
                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 168, Application US/08709209 Patent No. 5762938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                        TELEFAX: (212) 840-0712 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                FILING DATE: 21-AIG-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/105,483
FILING DATE: 12-AUG-1993
APPLICATION NUMBER: US 07/847,951
FILING DATE: 06-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Ker
CURRENT APPLICATION DATA:
APPLICATION NUMBER: USA
APPLICATION NUMBER: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA ZIP: 10036 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 55,506
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE TITLE OF INVENTION: STRAIN
                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              293 ctgtaatttttat 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Curtis, Morris & Safford ADDRESSEE: c/o William S. Frommer STREET: 530 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13;
                                                                                                                                                                                                                                                                                                                  Frommer, William S.
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                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Paoletti, Enzo
                                                                                                                                                                                                                                                                                                                                                                                                                                              21-AUG-1996
                                          100.0%; FI
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                                                                                                                                                                                                                                                                                     454310-2400
                                                           Score 13; DB 1;
Pred. No. 4.7e+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                             4.7e+03;
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                                                                           Length 39;
                                              Indels
                                            0;
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                                            Gaps
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US-08-303-275-56/c
                                                                                                                                                                                                                                                                                                                                                                                                        US-08-303-275-56
                                                                                                                                                 Sequence 1
Patent No.
                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 56, Appli Patent No. 5766598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (212) 840-0712 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/897,382
FILING DATE: 11-JUN-1992
ATTORNBY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 454310-2420 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                      APPLICANT
                                                   APPLICANT:
                                                                   APPLICANT:
                                                                                    APPLICANT:
                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Tartaglia, James APPLICANT: Cox, William I.
     APPLICANT
                   APPLICANT
                                                                                                                                                                                                                                                                   293 ctgtaatttttat 305
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CITY: New York
STATE: New York
                                                                                                                                                                                                                                                25 CTGTAATTTTAT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: UZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Curtis, Morris & Safford ADDRESSEE: C/O William S. Frommer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                    168, Application US/08458101
o. 5766599
                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/08303275
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                             Tartaglia, James
No. 5766599ton, Elizabeth K.
Riviere, Michel
                                                                               Perkus, Marion E.
Taylor, Jill
                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
de Taisne, Charles
Limbach, Keith J.
                                                                                                                  Paoletti,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Paoletti, Enzo
                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (212) 840-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMUNODEFICIENCY VIRUS RECOMBINANT POXVIRUS VACCINE
                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                  Enzo
                                                                                                                                                                                                                                                                                                                                                      4.0%;
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                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                     Score 13; DB 1;
Pred. No. 4.7e+03
                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                  Length 39;
                                                                                                                                                                                                                                                                                                                     Indels
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Pincus, Steven E. Cox, William I.

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                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                         Sequence 19, Application US/09028361A Patent No. 5962296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 45
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Relacement Application DATA:
APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Audonnet, Jean-Christophe Francis
APPLICANT: Gettig, Russell Robert
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
TITLE OF INVENTION: STRAIN
CURRENT APPLICATION DATA:
                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                     TITLE OF INVENTION: METHOD FOR CLONING AND TITLE OF INVENTION: PRODUCING THERMOMICROBITITLE OF INVENTION: POLYMERASE I IN E. COLI
                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          293 ctgtaatttttat 305
                            COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 530 Fi
CITY: New York
STATE: NY
               SOFTWARE:
                                                                                                                   COUNTRY:
                                                                                                                                      STATE:
                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                           25 CTGTAATTTTAT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
les 13; Conserv
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TOPOLOGY: lir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: UZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Curtis, Morris & Safford ADDRESSEE: c/o William S. Frommer STREET: 530 Fifth Avenue
                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                     01915
                                                                                                                                                   Beverly
                                                                                                                                   MA
                                                                                                                                                                    E: New England Biolabs, Inc
32 Tozer Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                   SD
                                                                                                                                                                                                                                                                                      ETTWILLER, LAURENÇE XU, SHUANG-YONG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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               FastSEQ Version 2.0
                                               IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (212) 840-3333
                                                                Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1995
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 39;
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RESULT 43
US-08-199-507B-39/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 39, Application US/08199507B Patent No. 5472841
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                 INFORMATION FOR SEQ ID NO:
                                                                                                                                  APPLICATION NUMBER: 07/53 FILING DATE: 11-JUNE-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
FILING DATE: 10-JUNE-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                     SOFTWARE: WordPerfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Williams, Gregory
REGISTRATION NUMBER: 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA: APPLICATION NUMBER:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 978-927-5054
                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 8400 E.
CITY: Englewood
STATE: Colorado
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/199,507B FILING DATE: 22 FEBRUARY 1994 CLASSIFICATION: 435
                                                                                                   NAME: Barry J. Swanson REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 ATATATTAATTAT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 atatattaattat 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid STRANDEDNESS: sing
                                               TELEPHONE:
                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH:
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                               (303)
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                                                 (303)
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100.0%;
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                                                                                                                                                                                                                                                                                                                                          MS-DOS
                                                                                                                                                                      07/536,428
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                                                                                                   33,215
                                                                                                                                                                                                                                                                                                                                                                            5.25 inch, 360 Kb storage
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Pred. No.
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LENGTH: 40 base pairs

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;; TYPE: nucleic acid
;; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-199-507B-39
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Best Local Similarity
Matches 13; Conserv
                                                        Query Match
Best Local Similarity
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                                              Matches
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                                                                                                                                                                                                                  ATTOKNUL.

NAME: Barry J. Swall.

REGISTRATION NUMBER: 33,215

REFERENCE/DOCKET NUMBER: NEXT

TELECOMMUNICATION INFORMATION:

TOTAL PHONE: (303) 793-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                        TELEFAX: (303) 793-343
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskettu
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: JAYASEN?
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/199,507
FILING DATE: 22 FEBRUARY 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                               FILING DATE: 11-JUNE-1990 ATTORNEY/AGENT INFORMATION: NAME: Barry J. Swanson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157 ggaaaatataaat 169
                                                                                                                                           LENGTH: 40 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: WordPerfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 80111
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                                            Conservative
                                                                                                                                  linear
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)0 E. Prentice Avenue, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Diskette, 3.50 inch, 1.44 MB
                                                          4.0%;
100.0%;
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NUCLEIC ACID LIGAND INHIBITORS
OF HUMAN NEUTROPHIL ELASTASE
: 59
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100.0%; Pred. No.
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                                                        Score 13;
Pred. No.
                                              Mismatches
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                                                          DB 1; L. 4.7e+03;
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Search completed: January 24, Job time: 3711 sec
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                                                                                                                                                              Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 41 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: WENDEROTH, LIND & PONACK, L.L.P.
STREET: 2033 K Street, N.W. - Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: GB 9506782.3
FILING DATE: 01-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB96/00776
FILING DATE: 01-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                        TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 202-721-8200
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                 251 ttcaggggggaat 263
                                                                                                                                                                                                                                                                                                        LENGTH: 41 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: OGCLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Warren M Cheek, Jr. REGISTRATION NUMBER: 33,367 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 202-721-8250
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Pred. No.
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Title:
Perfect score:
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327
1 atttgggatatcttaaattt.....tttcatgttttcttattgtt 327
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.
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	Match Len 4.9 4.0 4.3 4.3 4.3 4.3 4.3 4.3 4.3 4.3 4.3 4.3
	9th 0 229 336 3329 3 36 3 37 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
ALIGNME	ARO99868 ARO19036 ARO19036 ARO19036 ARO19036 ARO19036 ARO28182 ARO28182 ARO28182 ARO29985 ARO99855 AXO49974 AXO49975 AXO49975 AXI37975 AXI37975 AXI37975 AXI37976
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	ALIGNMENTS

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Method for detecting foreign DNA fragment insert in Vero toxin gene Patent: JP 1999243996-A 3 14-SEP-1999;

TOYOBO CO LTD

OS Unidentified
PN JP 1999243996-A/3
PD 14-SEP-1999
PF 27-FEB-1998 JP 1998047677
PR MASAHIRO KUSUMOTO, YOSHIAKI NISHIYA, YOSHIHISA KAWAMURA, PI KUNIHIRO SHINAGAWA
PC C1201/68, C12N15/09/(C12N15/09,C12R1:185),C12N15/00, CC Strandedness: Both;
CC Strandedness: Both;
CC Topology: Linear;
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Telomeric repeats (TTAGGC)n
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
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C.elegans DNA fragment with
X97532
X97532.1 GI:1296496
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16; Conserv
                                                            Wicky, C., Villeneuve, A.M., Lauper, N.,
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                                       Muller, F
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          are sufficient for chromosome capping
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                                                            Codourey, L., Tobler, H. and
                                                                                                              Caenorhabditis.
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Best Local Similarity
Matches 16; Conserv
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AR019036
                                                                                                      Sequence
AR014030
Unclassified.

1 (bases 1 to 27)

Keene, J.D., Levine, T. and Gao, F.

Methods and compositions useful in the recognition, binding and expression of ribonucleic acids involved in cell growth, neoplasia
                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 36)
Noriega,F.R. and Levine,M.M.
Gua mutants of shigella spp. and vaccines
Patent: US 5783196-A 16 21-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          function in Caenorhabditis elegans
Proc. Natl. Acad. Sci. U.S.A. 93 (17), 8983-8988 (1996)
96392352
                                                         Unknown
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/db_xref="taxon:6239"
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I21980
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Behnke,D., Schlott,B., Albrecht,S., Guhrs,K. and Hartmann,M. Expression of signal-peptide-free staphylokinases
Patent: US 5801037-A 29 01-SEP-1998;
                                                                                                                                               Unknown
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Keene, J.D., Levine, T. and Gao, F.

Methods and compositions useful in the recognition, binding and expression of ribonucleic acids involved in cell growth, neoplasia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unknown
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Patent: US 5525495-A 66 11-JUN-1996;
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                                                                                                                                                                                                                    Unclassified.
1 (bases 1 to 29)
Williams, J.A. and Byrne, L. Marie.
Compositions for the prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20
AR076353
                                                                                                                                                                                                   Patent: US 6080400-A 12 27-JUN-2000;
                                                                                                                                                                                                                                                          Unknown
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Bennett, C. Frank, Ackermann, E.J. and Cowsert, L.M.
Antisense inhibition of cellular inhibitor of apoptosis-1
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E27913
         1 (bases 1 to 32)
Masahiro,K.Y.N.N. and Kawamura,K.S.
Method for detecting foreign DNA fragment insert
Patent: JP 1999243996-A 3 14-SEP-1999;
                                                                                                                                                                                                                                                                                                                                         Mutated forms of the ataxia-telangiectasia screen for a partial A-T phenotype Patent: US 6200749-A 110 13-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ataxia-telangiectasia gene and its genomic organization Patent: US 5858661-A 31 12-JAN-1999; Location/Qualifiers
TOYOBO CO LTD
                                                                                   E27913.1 GI:13020766
JP 1999243996-A/3.
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AR063204
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AR019036
1 (bases 1 to Hudson, P. John,
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Noriega,F.R. and Levine,M.M.
Gua mutants of shigella spp. and vac
Patent: US 5783196-A 16 21-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KUNIHIRO SHINAGAWA

PC. C12Q1/88,C12N15/09//(C12N15/09,C12R1:185),C12N15/00,
CC.12R1:185)
CC. Strandedness: Both;
CC. Topology: Linear;
CC. Topology: Linear;
CR. Topology: Line
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JP 199243996-A/3
14-SEP-1999
27-FEB-1998 JP 1998047677
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3 c 10 g
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Lah, M.,

Kortt, A. Andrew, Irving, R. Alexander,

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SOURCE
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                                 1 (bases 1 to 45)
Bout.A., Havenga.M.J. and Vogels.R.
Adenovirus derived gene delivery vehicles comprising element of adenovirus type 35
Patent: WO 0070071-A 75 23-NOV-2000;
Introgene B.V. (NL)
                                                                                                                                                                Sequence 75 from Patent Ax049974
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adenovirus derived gene delivery vehicles element of adenovirus type 35 patent: WO 0070071-A 74 23-NOV-2000;
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                                                                                                                               synthetic construct.
                                                                                                                                                    AX049974.1 GI:12226351
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                                                                                                       artificial sequence.
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/db_xref="taxon:32630"
/note="oligonuclectide TATA-plus"
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                                                                                                                    Schouten, G.J., Vogels, R. and Ops
Modified adenoviral vectors for
                                                                                                                                           artificial sequence.
1 (bases 1 to 45)
                                                                                                                                                                    synthetic construct
synthetic construct
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1 (bases 1 to 45)
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                                                                                            Patent: WO 0120014-A 5 22-MAR-2001; Introgene B.V. (NL)
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Pred. No. 6e+04;
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                                                                                                                                                               synthetic construct synthetic construct
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1 (bases 1 to 45)
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1 (bases 1 to 45)
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AX137976
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                                                                                                Introgene B.V. (NL)
                                                                                                         Modified adenoviral vectors for use Patent: EP 1083229-A 5 14-MAR-2001;
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/db_xref="taxon:32630"
/note="primer"
          /note="'Primer TATAmin'"
7 c 5 g 14
                                         /db_xref="taxon:32630"
/note="primer"
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AX159856
                                                                                                                               1 (bases 1 to 18)
Cochran,M.D. and Junker,D.E.
Recombinant swinepox virus
Patent: US 6221361-A 13 24-APR-2001;
                                                                                                                                                                                                                                                   AR146953 18 bp
Sequence 13 from patent
AR146953
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Nucleic acids containing single nucleotide
methods of use thereof
Patent: WO 0140521-A 3184 07-JUN-2001;
Curagen Corporation (US)
                                                                                                                                                                                     Unclassified
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae
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/db_xref="taxon:9606"
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Accession number cg43063075"
                                                                             /organism="unknown"
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L00.0%; Pred. No. 1.6e+05;
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AR121058
Sequence 35 from Pata
A97479
A97479.1 GI:6780825
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                                                                                                                                                                                                                                                                                   Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus
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/db_xref="taxon:10407"
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RESULT 27
AX164353
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AX164353
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13; Conserv
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Gala, J. and Vannuffel, P.
GENETIC SEQUENCES, DIAGNOSTIC AND/OR QUANTIFICATION METHODS AND
DEVICES FOR THE IDENTIFICATION OF STAPHYLOCOCCI STRAINS
PATENT: WO 9916780-A 35 08-APR-1999;
GALA JEAN LUC (BE); UNIV LOUVAIN (BE)
synthetic construct.
synthetic construct
artificial sequence.
                                                                                                                                                                                                                                                                                                                                             Patent: WO 0118198-A 74 15-MAR-2001;
CENTRE NATIONAL DE LA RECHERCHE SCIE
Location/Qualifiers
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AX093544
                                                   AX164353.1
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Patent: WO
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Weissenbach, J. and Hazan, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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183 from Patent
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/db_xref="taxon:9606"
/note="Site accepteur d' pissage
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Pred. No. 1.6e+05;
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WO0118198.
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A bac-based sts-content map spanning a 35-mb region of human chromosome 1p35-p36
Genomics. 74 (1), 55-70 (2001)
                                                                13;
                                                                                                                                                                                                                                                                                                            Submitted (04-AUG-2001) Akira Horii, Tohoku University School of Medicine, Wolecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai, Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp, Tel:81-22-717-8042, Fax:81-22-717-8047)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Loci for idiopathic generalized epilepsy, mutations thereof and method using same to assess, diagnose, prognose or treat epilepsy Patent: WO 0138544-A 183 31-MAY-2001; McGill University (CA)
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                                                                                                                                                                                                                                                                                                                                                                                                           Horii, A.
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/db_xref="taxon:33630"
/note="synthetic oligonucleotide"
/note="synthetic oligonucleotide"
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/db_xref="taxon:32630"
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AX042574/c
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w synthetic construct
artificial sequence.
1 (bases 1 to 25)
Ulfendahl, P.J. and Wong, K.C.
Primers for identifying typing or class
Patent: WO 0065088-A 140 02-NOV-2000;
Amersham Pharmacia Biotech AB (SE)
                                                                                                  ATTGTAAAAAAAA
AX039624
Sequence 13
AX039624
AX039624.1
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 834 from Patent AX043268
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13; Conserv
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Location/Qualifiers
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1 (bases 1 to 25)
Ulfendahl, P.J. and wong, K.C.
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Sequence 140 from Patent
AX042574
AX042574.1 GI:11341182
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nilarity 100.0%;
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/db_xref="taxon:32630"
/note="DQA1 Homozygote primer sequence"
1 5 c 3 g 13 t
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/db_xref="taxon:32630"
/note="DQA1 Heterozygote Primer Sequence"
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1 (bases 1 to 26)

Hernstadt,C. and Davis,R.E.

Single nucleotide polymorphisms in mitochondrial genes that segreg

ate with alzheimer's disease

patent: WO 0063441-A 13 26-OCT-2000;
Unclassified.
1 (bases 1 to 28)
                    Unknown.
                                                             Sequence 64 from patent US AR014028
                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 26)
Herrnstadt,C. and Davis,R.E.
Single nucleotide polymorphisms in mitochondrial genes that segreg
ate with alzheimer's disease
                              Unknown.
                                                                                                                                                                                                                                                                                                                                                                            synthetic construct. synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 43 from Patent W00063441.
                                                   AR014028.1
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Similarity 100.0%;
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/db_xref="taxon:32630"
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/db_xref="taxon:32630"
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Sequence 26
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13; Conserv
                                                                    artificial sequence.

1 (bases 1 to 29)
Burtscher, H.D., Mueller, R.D., Hoelke, W.D.
High active alkaline phosphatase
Patent: EP 0955369-A 26 10-NOV-1999;
ROCHE DIAGNOSTICS GMBH (DE)
                                                                                                                                                                 synthetic construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and immunoregulation
Patent: US 5525495-A 64 11-JUN-1996;
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Keene, J.D., Levine, T. and Gao, F.
Methods and compositions useful in the recognition, bindi
expression of ribonucleic acids involved in cell growth,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Keene, J.D., Levine, T. and Gao, F. Methods and compositions useful expression of ribonucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and immunoregulation Patent: US 5773246-A 64 30-JUN-1998;
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Artificial"
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Pred. No. 1.6e+05;
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Werner, H.R. M.M. and Burutosha, J.L.M.M. Highly active alkaline phosphatase Patent: JP 199332586-A 23 07-DEC-1999; Patent: JP 199932586-A 23 07-DEC-1999; Patent: JP 199932586-A/23 PD 07-DEC-1999 JP 199126494 PR 05-MAY-1998 DE 19819962:7

PI WERNER HOERUKU, REINA MULLER, HERUMUTTO
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C12N15/00,C12N5/00
C12N15/00,C12N5/00
CC
CC
FH Key
FT Source
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Highly active alkali
E59972 GI:1301774
JP 1999332586-A/23.
                                                                                                          AR028230
Sequence
AR028230
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              Shiloh,Y.
Ataxia-telangiectasia gene and its genomic organization Patent: US 5858661-A 79 12-JAN-1999;
                                                        Unclassified
                                                                  Unknown
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                                                                                                AR028230.1
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ilarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                         WERNER HOERUKU, REINA MULLER, HERUMUTTO BURUTOSHA, PI
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/db_xref="taxon:32644"
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1. .29
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                                                                                                                   from patent US 5858661.
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15 AAAAATTATTTC 27
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Local Similarity 100.0%; Pred. No. 1.6e+05;
hes 13; Conservative 0; Mismatches 0;
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                                                                                                                                                              synthetic construct artificial sequence.

1 (bases 1 to 30)

Nazarenko,I. and Rashtchian,A.
Improved primers and methods for the detection and discrimination of nucleic acids
                                                                                                                          Patent: WO 0079009-A 42 28-DEC-2000;
Life Technologies, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mutated forms of the ataxia-telangiectasia screen for a partial A-T phenotype Patent: US 6200749-A 158 13-MAR-2001;
                                                                                                                                                                                                                                         synthetic construct
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158 from
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42 from Patent WO0079009.
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195122
195122.1 GI:3939592
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Cell 37, 2
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                                                                                                                                                                                                                              Structural requirements for the
                                                                                                                                                                                                                                                   Amphibia; Batrachia; Xenopodinae; Xenopus.

1 (bases 1 to 33)
                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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K01606
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11 c 7 g
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/db_xref="taxon:8355"
4 c 2 g 19
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Other publication JP 6343469 9.
Other publication CA 2124272 9.
Other publication CN 1098744 9.
Other publication DA 4317845 9.
Other publication DE 4317845 9.
Other publication ZA 9403730 9.
AX167671
Sequence
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Sequence
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13; Conserv
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Schreier, P.H., Stenzel, K.D., Adam, G.I
DNA coding for plant virus sequences
Patent: EP 0626449-A 14 30-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14 from Patent A41027
                                                                                                                                                                                                                             DNA comprising plum pox virus and tomato for disease resistance Patent: US 5973135-A 14 26-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent:
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5 c 5 g
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  from Patent W00144277.
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Search completed: January 24, 2002, 03:22:36 Job time: 3813 sec
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1 (bases 1 to 36)

1 (bases 1 to 36)

Schreier, P.H., Stenzel; K., Adam, G. unter and Maiss, E.

Schreier, P.H., Stenzel; K., Adam, G. unter and Maiss, E.

DNA comprising plum pox virus and tomato spotted wilt virus cDNAS

for disease resistance
Patent: US 559823-A 14 29-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14 from patent US 5569823. I28261 I28261.1 GI:1819037
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1 (bases 1 to 36)

1 (bases 1 to 36)

wegrich Glover,L., Budziszewski,G.J., Levin,J.Z. and Zhou,Q.

Herbicide target genes and methods

Patent: WO 0144277-A 16 21-JUN-2001;

Syngenta Participations AG (CH)

Location/Qualifiers

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Listing first 45 summaries
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SUMMARIES

/organism≖"Clostridium perfringens"

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	immunogenic	group; Clostridiaceae;		24-AUG-2000		luman re	Human D	HOm	Hom	HOI	Homo sap	Ноп	AJ011856 Saccharom AC093220 Homo sapi	Home	~ -	Homo	Home	Homo	Huma	Huma Plas	Plas	acch	Plasmodiu	Home	AL049184 Plasmodiu	Dict	Pla	HOme	Pla	Seq	l Sequ	Description	

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Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
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Gibert,M., Jolivet-Reynaud,C. and Pc
Beta2 toxin, a novel toxin produced
Gene 203 (1), 65-73 (1997)
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Gibert, M. and Popoff, M.R.
Clostridium toxin, and me
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Pred. No. 2.8e-28;
; Mismatches 0;
                                                                                                                                                                                     method
                                                                                                                                                                                  for preparing
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                                                                                                 perfringens'
                                                       product"
                                                                                                                                         (FR)
                                                                                                                                                                                                                                                                                                                                         PAT
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                                                                                                                                                                                   immunogenic
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translation="MKKIISKFTVIFMFSCFLIVGAISPMKASAKEIDAYRKVMENYL"

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REFERENCE
AUTHORS
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                     SOURCE
ORGANISM
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AP003515
                                                                                                                              FEATURES
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                               VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                TITLE
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Best Local
                            gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gatatattaattatatagctgaaaatttataattatatgataagtatagttaataaataa 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTTGGGATATCTTAAATTTAGCACAGAAGAATGTTTAAATGAAATAAAGATAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   327;
                                                                                                                                                Submitted (12-APR-2001) Tohru Shimizu, Institute of Basic Medical Sciences, University of Tukuba, Department of Microbiology; 1-1-1 Tennohdai, Tsukuba, Ibaraki 305-8575, Japan [E-mail:tshimizu@md.tsukuba.ac.jp, Tel:81-298-53-3354,
                                                                                                                                                                                                                                                   Complete Nucleotide Sequence Clostridium perfringens Unpublished
                                                                                                                                                                                                                                                                            1 (bases I to )*****, Ohtani,K., Ohshima,S., Hirakawa,H., Ohshima,K. Shimizu,T., Hattori,M., Kuhara,S., Hayashi,H. Shimizu,T., Winalantide Sequence of the Virulence
                                                                                                                                                                                                                                                                                                                                                                   Clostridium perfringens (strain:13) plasmid:pCP13 DNA Clostridium perfringens
                                                                                                                                                                                                                                                                                                                                                                                                                           AP003515 54310 bp
Clostridium perfringens
AP003515
                                                                                                                                            Fax:81-298-53-3354
                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                         Clostridium.
                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                              AP003515.1
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WYKTEFLNGAIYDMEFTYSSKOGKLIVSDMERTYVENBEGKYLLFPSFRTQVCTWDDEL
AQAIGGVYPQTYSDRETYYADNILLNFRQYATSGSRDLKVEYSVVDHWMWKDDVKASQ
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115 c 209 g 462 t
/gene="soj"
940. .1692
                            /note="anaerobic 940. .1692
                                                                                  /organism="Clostridium
/plasmid="pCP13"
                                                      /db_xref="taxon:1502"
                                                                      /strain="13"
                                                                                                                 1. .54310
                                                                                                                           ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                              GI:15076712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
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Pred. No. 2.8e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA circular BC9 plasmid pCP13 DNA,
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                                         pathogen
                                                                                                 perfringens
                                         for gas gangrene"
                                                                                                                                                                                                                                                                                                            Ohshima, K.,
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                                                                                                                                                                                                                                                                                                                                                      group; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                        complete sequence.
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  and Shimizu,T.
e Plasmid pCP13 1
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protein from
aa overlap
truncated"
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4040. .4222
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/CIDATES ACTION "MAKKFSISEGMLNGISKNTRKVEEFQAKENFKIEVINIDRIKRN
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KIRDIIANDLNLSATQVGRYEBINNKLIPELKAVIEGGNLTIANASEFSSLSEENQRV
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LKSENENLKKKLDSNNIEEERKEIEGGIKIEFEEKLKNEKVILEEELKRKYDKKIEDI
TKEAKENNLEKQRLKDELSKLKEKSNNEVDIKNTKENFVLVQNLKLIDNSFKNLKSQI
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1751. .3031
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/transl_table=11
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/protein_id="BAB62442.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      overlap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="PCP04"
3773. .4024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CFFYIEDKAIKISKEKQSEEAKEKTISFSKTSTKTYLNNKWLEYLGVSEDERSCIIEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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LGYEKNLTNQFYNSRNGYSKKTIKSELGTITLNILRYRN"
                                                                                                                                                                                                                                                                                                                                                                                                                                       truncated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from Yersinia
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/gene="PCP04"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /transl_table=11
/product="ParB protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCP02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="426 aa, similar to gpu:AF300944_3 presumptive ParB
protein from Lactococcus lactis subsplactis (242 aa); 30%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VVESTFEECPVVFSSKKARASLNYKDLSKEIF"
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RSQQNRLAKALEEI EDKYDYCLIDCPPALNMI TVNALCASDEVLVPI KIDKFALDGLE
YLLDSI EEIKDEFNPNLNFKGCFI TMDSSTTVNKVI KQELKSVLGEKMFNTSI HQNI K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ParA tamily"
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                                                                                                            /note="60 aa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="83 aa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="120 aa, no significant homology"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene="PCP03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene≖"PCP03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="426 aa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dentity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .3509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            266 aa overlap
                                                                                , similar to Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similar to pir:T14710 probable transposase pestis (402 aa); 44% identity in 50 aa
                                                                             gp:AF143819_1 transposase-like
coli (402 aa); 38% identity in
                                                                                60
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gene

CDS

gene

CDS

gene

CDS

gene

CDS

gene

CDS

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LFIVQIENEQILDKLIEDLKSESIIVQKRVMGDSSQYNTETLKIILVVCFIGLIFMIF
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WKFMLELICIYSIMIIFTIVSVIIPYILVSKIITLSNIIKNKPPKSIIILNSIVKVIL
ASIILIFFSNALDDLSSIGKGYEKNYKVWEETMQYYLLDELGFNDESIQSFSIEEMEK
LBAVYLLFNKQGAILADFNRYEPTSMEEAKOMLPEETMRETIIVPNYLLKHKVYVDV
                                                                                                                                                                                                                                                    GNIINISEDEKDRILLVPEKYRNFEKEILEYYGYNSQEPCSSTTCSHKTADGKLNLVE
QKQKIIWMKSNQKYFSYLLDVNPEEGNYVTDPIVSVLTESNDKLVSYYKIIGYNNSPF
KIRANSEEEVINGLEKYYDMSYYLIDPYNLYDNVASTIINIKAKVKVIIFAIVILLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(5804.
/gene="PCP08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MNIIEISNLNKKYFDKVIFKDFSLSIKKGEMIAISGRSGCGKSTLLNMIGLIEKFDSGEIIIDGVKNIKINSKLANKFLREKISYLFQNFALVDEETVEENLRLAIKHTIKNTKKIEBEIIRCLKFVGLEGCQKNYIYELSGGEQQRVAIARLMLKPSEI
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4588. .4746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  661 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="720 aa, similar to gp:AP001508_3 BH0280 product from Bacillus halodurans (713 aa); 23%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(5804. .7966)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="probable ABC transporter"
/protein_id="BAB62445.1"
/db_xref="GI:15076720"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function="ATP-binding protein"
note="211 aa, similar to gp:A89001508_4 ABC transporter
(APP-binding protein) from Bacillus halodurans (213 aa);
49% identity in 214 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(5169..5804)
/gene="PCP07"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="probable transposase"
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                                                                                                                                                                                                               INITYFTLILVVIELVFITFNINSLEKKNLIKVIKGEY"
                                                                                                                                                                                                                                     ISIIIILQNTSLYFNQNKNKIIVKKLHGYRLIYRYMNYFIMVLITWTCPLAIASLITKD
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                                                                                                                                                                   /gene="PCP09"
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                                                           transl_table=11
                                                                                      /codon_start=1
                                                                                                       /note="103 aa, no
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13459 ATAGAATTTTAACTCATGTTTTAAAAGTTAAATATATATTTTAAATTTAAAGTGTCCCAC 13518
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                                                                                                                                                                       Salzberg,S., Zhou,L., Sutton,G.G., Clayton,R., White,O., Smith,H.O., Fraser,C.M., Hoffman,S.L. et,al. Chromosome 2 sequence of the human malaria parasite Plasi
                                                                                                                                                                                                                                Gardner, M.J., Tettelin, H., Carucci, D.J., Cummings, L.M., Aravind, L., Koonin, E.V., Shallom, S., Mason, T., Yu, K., Fujii, C., Pederson, J., Shen, K., Jing, J., Aston, C., Lai, Z., Schwartz, D.C., Pertea, M.,
                                                                                                                                                                                                                                                                                                                                                                                           complete sequence.
AE001429 AE001362
AE001429.1 GI:3845321
                                                                                                                                                                                                                                                                                                                                                                                                                                                AE001429 12900 bp DNA
Plasmodium falciparum chromosome
Submitted (02-NOV-1998) The Institute for
                Direct Submission
                                      Gardner, M.J
                                                                           4;282(5395):1827
                                                                                             Erratum: [[published erratum
                                                                                                                    99021743
                                                                                                                                    Science 282 (5391), 1126-1132 (1998)
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QAQSSKFYCGEQKHRATARVKVGTTLYEAKDIKDAKLTAHAQTKYYKGVTEWNSYYAH
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/transl_table=11
/product="probable transposase"
/protein_id="BAB62448.1"
/db_xref="GI:15076723"
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Yersinia pestis plasmid pMT1 (402 aa); 25% identity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blakey,S.

Birect Submission
Direct Submission
Submitted (14-APR-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Mar 15, 2000 this sequence version replaced gi:7210154.
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                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 39347)
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Human DNA sequence from
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AL135906.19
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DIANKFTKALAGIYFFFSSSIENAGVSGVTIFYWDSMRMASIASSTINPYGIAALVLI
VLVVVLIVLYIWLYRRKKSWKHECKKHLST"
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/protein_id="AAC71980.1"
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/db_xref="G1:3845322"
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MKSRRLAEIQLPKCPHYNNDPELKKIIDKLNBERIKKYIETNNSFEELHGLLVKERTK
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/codon_start=1
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/note=":3
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/db_xref="taxon:5833"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The following abbreviations are used to associate primary access; numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at attp://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chromosome 6, constructed by the Sanger Centre Chromosome 6 Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     corresponding to the overlapping clone, as we submit sequences only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence has been finished according to sequence map criteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  feature key.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="L1 6091. .816
                                                                                                                                                                                      10657.
                                                                                                                                                                                                                                                                                                                                   8959
                                                                                                                                                                                                                                                                                                                                                                                                                          8287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="MER47A repeat: matches 13.
4779. .5831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4214.
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  16886.
                                                                                                                                                                                                                                    10091.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6028.
                                                16821.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
/clone="RP1-20N11"
                                                                                              16682
                     note="20 copies 2 mer ta
                                                                    note="L1P3"
                                                                                                                                          /note="L1PA2 repeat:
11432. .16672
                                                                                                                                                                                      /note="L1M2 repeat:
10657. .11436
                                                                                                                                                                                                                                                       note="L1 repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="L1M2 repeat: matches 1528. .2663 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="AluY repeat: matches 1. .311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="L1M3c repeat: matches 999. .1402 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="L1PA12 repeat: matches -1421. .-291 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                  'note="L1PA2 repeat: matches 900.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone_lib="RPCI-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .39347
                                                                                                                                                                                                                                                                                                                                                                              . 8965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .8167
                                                                                                                                                                                                                                                                                                                                                                                                                            . 8567
                                                                                                                                                                                                                                                                                                        L1M3c repeat: matches 1092.
                                                                                                                                                                                                                                                                                                                                                                                                  AluSx repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                           L1PA15 repeat: matches 4085. .6157 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L1M3c repeat: matches 1402.
                                                                                                                                                                                                                                                                                                                                                    l repeat: matches 2737. .2901 of consensus"
                                                16860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat:
                                                                 repeat:
                                                                                                                                                                                                                                                            matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            matches 2729. .2777
                                                                                                                                                                                                              matches 5115.
                                                                    matches 5677.
                                                                                                                                                           matches 3. .776 of consensus*
                                                                                                                                                                                                                                                                                                                                                                                                  matches 3.
                        90% conserved'
                                                                                                                                                                                                                                                       2903.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 associate primary accession their source databases:
                                                                                                                                                                                                                                                          .3922 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                  .284 of consensus"
                                                                                                                  .6146 of
                                                                                                                                                                                                              . 5687
                                                                    .5791
                                                                                                                                                                                                                                                                                                        .1236 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .1610 of consensus"
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repeat: matches

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.152 of consensus"

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BASE COUNT
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Best Local Similarity
Matches 157; Conserv
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Conservative
                                                                                                                                                                                                                                                     /note="LIPAl3 1 36726. .37022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17036. .17343

/note="MER4A repeat: matches 367.

17377. .17678
                                                                                                                                                   /note="TIGGER2 repeat: matches 2448.
7155 c 6738 g 11025 t
                                                                                                                                                                                                                     /note="AluY repeat: matches 3. 37033. 38914
                                                                                                                                                                                                                                                                                                                                                                                                                                 33046
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="52 copies 2 mer tt 64% conserved" complement(32852 .33057)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(32119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="L1M4 repeat: matches 862. .2044 of consensus"
31742. .32332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="LIMB6 repeat: matches 5552. .6128 of consensus" 29885. .31038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="133 copies 2 mer aa 54% conserved" 29274. .29834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BamHI and EcoRI bot suggest approx 200bp missing complement(26230. .26730) /note="match: GSS: Em:B69019"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(20068. .20528)
/note="match: GSS: Em:AQ218253"
                                                                                                                                                                                       /note="L1PA13 repeat: 39090. .39341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(26267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="12 copies 2
25570. .25754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23091.
                                                                                                                                                                                                                                                                                                                                                            /note="L1PA7 repeat: matches 4855. .6127
34564. .34625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="match: GSS: Em:AQ078965"
32769. .32872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="L1MD1 repeat: matches 5317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="LIME2 repeat: matches 5094.
28440. .28705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="match: GSS: Em:AQ230058"
27019. .27243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25879. .26639
/note="Tandem repeat. Tandem repeat contains forced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="AluYb8 repeat: matches 1. .318 of consensus"
17997. .18193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="LlMA9 repeat: matches 5783.
17679. .17996
                                                                                                                                                                                                                                                                                                                                                                                                                                               note="match: GSS: Em:AQ780759"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="LTR40a repeat: matches 282.
27306. .28098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="398 copies 2 mer aa 58% conserved'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="AluJo/FRAM repeat: matches 173. .291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="L1PA4 repeat: matches 5999. .6146 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="MLT1I repeat: matches 370.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="LIME repeat: matches 429. .1193
                                                                                                                                                                                                                                                                                                        note="14 copies 2 mer ac 89% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="L1MA9 repeat: matches 6112.
                                                                 24.2%;
54.7%;
                                                                                                                                                                                                                                                                                                                                                                                              ="41 copies 2 mer tt 73% conserved"
. .34362
                                                                                                                                                                                                                                                                                            .36725
                                                                                                                                                                                                                                                                                                                            .34664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 25553
                                                                                                                                                                                                                                                                                                                                          copies 2
                                                   0;
                                                                 Score 79; DB 9
Pred. No. 0.43;
                                                                                                                                                                                                                                                                          repeat:
                                                 Mismatches 130;
                                                                                                                                                                                                                                                                                                                                            mer ta 71% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mer ca 95% conserved"
                                                                                                                                                                                                       matches 4198.
                                                                                                                                                                                                                                                                          matches 2266.
                                                                                   DB 9; Length 39347
                                                                                                                                                                                                                                        . 308
                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .5893 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .5922 of
                                                                                                                                                                                                                                        of consensus"
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ataaatgaaaaaaattatttcaaagtttactgtaatttttatgtttt 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aatttataattatatgataagtatagttaataaataaaaagtgttctcggggggacacttt 143
                                                                                                                                                                                                                                              Submitted (14-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 13, 2000 this sequence version replaced gi:6970502. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 53932)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-21D18
                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished 2 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens clone
                                                                                                                                                                                                                    http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTG; HTGS_PHASEO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC023371.2 GI:9123990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 53932)
Center project Information Center project name: L3985 Center clone name: 21_D_18
                                                                             Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                      Center code: WIBR
                                                                                                                                                                      Center: Whitehead Institute/ MIT Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53932 bp DNA
s clone RP11-21D18, LOW-PASS
                                                                                                                                                                                             Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE SAMPLING
                                                                                                                                                                      for Genome
                                                                                                                                                                         Research
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sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows
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9 4769: cu..

70 4869: gap of

870 5739: contig of 8

5740 5839: gap of

5840 6703: contig of

6704 6803: gap of

7075: contig of

contig of

contig of
                                                                 29074
                                                                                                                                                                                                                                                                              88 19361: contig of 874 b)
62 19461: gap of 100 bp
62 20326: contig of 865 b)
27 20426: gap of 100 bp
27 21291: contig of 869 b)
92 21391: gap of 100 bp
92 22381: contig of 890 b)
82 22381: gap of 100 bp
82 23371: gap of 100 bp
72 23371: gap of 100 bp
72 23371: gap of 100 bp
73 24349: contig of 878 b)
74 24349: contig of 878 b)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 11672: gap of 10
13238: contig of 8
19 12628: gap of 10
13488: contig of 8
19 1388: gap of 10
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10 9739: gap of

0 10613: contin 1
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6 8671: contig of
2 8771: gap of 10
2 9639: contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0 969: gap of
0 1815: con
6 1915: gap of
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3 2897: gap
30155: gap of 1
31136: contig of
                                                               29173:
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                   28086: contig of 18186: gap of 192073: contig of 19173: gap of 19155: ga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4569: gap of 10
15452: contig of 10
5552: gap of 10
16429: contig of 10
5529: gap of 10
17401: contig of 10
7501: gap of 10
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262: gap of
27122: contig of
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3768: con
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8387: contig of 886 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4469: contig of
                                                                                                                                                                                                                                                               gap of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           not be assumed that this clone to completion. In the event that
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of 869 bp in length
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of 860 bp in
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BASE COUNT
ORIGIN
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                                                                               source
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                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
                                   /clone_lib="RPCI-11 Human 9672 c 9208 g 15109
                                                                                        Location/Qualifiers
                                                    clone="RP11-21D18"
                                                                                                                                           51081:
                                                                                                                                                                                                 48153:
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46090: contig of
46190: gap of 1
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32116: contig
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39164: contig of 901 b
1264: gap of 100 bp
40131: con+17
                                                                                                                                                                                                                                                          100 bp
14109: contig of 880 bp
1209: gap of
100 km
45090: con+1
                                                                                                                       1133: gap of 100 bp

50009: contig of 876 b

11009: gap of 100 bp

50981: contig of 872 b

1081: gap of 100 bp

51957: contig of 876 b

51957: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                           1/U: gap of
35169: con+
                                                                                               52945: contig of 888
045: gap of 100 1
53932: contig of 887
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37135: contig of 871
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...contig of 867 bp:
...contig of 883 bp:
...contig of 893 bp:
...contig of 898 bp:
                                                                                                                                                                                       contig of 880
                                                                                                                                                                                                       contig of 881
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В 24 В B Qy Best Local Similarity 55.3 Matches 173; Conservative Query Match Best Local 71 ttatatagotgaaaatttataattatatgataagtatagttaataaataaaaagtgttct 130 14 taaatttagcacagaagaatgtttaaatgaaataaagataataaaaagatatat---taa 70 cgggggacacttttttgttttaaaaaggaaaaatataaaataaaatttagataaaagtgtaa 190 23.8%; Score 77.8; DE Pred. No. 0.55; 0; Mismatches .55 138; Indels Ψ Gaps 42773

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* NOTE: This is a 'working draft' sequence. It currently

* consists of I contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* This sequence will be replaced
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Submitted (05-JAN-1999) Stanford DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 163443)
Hyman, R.W., Fung, E.L., Qin, F., Rowley, D., Mao, J.,
Kurdi, O.B., Conway, A.B. and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94304, USA
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1 163443: contig of 163443 bp in length.
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/db_xref="taxon:5833"
/chromosome="12"
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SEQUENCING
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                 61 gatatattaattatatagetgaaaatttataattatatgataagtatagttaataaataa 120
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                                                                                         atttgggatatcttaaatttagcacagaagaatgtttaaatgaaataaagataataaaaa 60
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* NOTE: This is a 'working draft' sequence. It currently

* consists of 4 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (21-AUG-1998) Stanford DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hyman, R.W., Qin, F., Fung, E.L., Conway, A.B. and Davis, R.W. Direct Submission
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Hyman, R.W., Fung, E.L., Qin, F., Rowley, D.,
Kurdi, O.B., Conway, A.B. and Davis, R.W.
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Plasmodium falciparum chromosome 12
PROGRESS ***, 4 unordered pieces.
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/organism="Plasmodium
/db_xref="taxon:5833"
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/clone="PFYAC357"
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                                                             173;
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Direct Submission
Submitted (26-AUG-2000) Biochemistry, National Cheng
Submitted (16-AUG-2000) Biochemistry, National Cheng
Submitted (16-AUG-2000) Biochemistry, National Cheng
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                                                           Conservative
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                                                                                                                                                                              /product="putative transcription factor StkA"
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                                                                                                                                                                 COYLE, A.D. CHENDAULY, I. CHENDAULOS, C. CENER, A.D. CHENDAULOS, C. COYLE, M.D. Dathorne, S.R., David, R., David, R., David, C., Davis, C., Davis, C., Dathorne, S.R., David, R., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwalte, K. J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagy, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Homaris, C., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Hubez, J., Hulyk, S., Lume, J., Jackson, E., Kelly, S., Khan, U., King, L., Korvah, J., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Loulseged, H., Lozado, R., J., Lu, J., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucler, R., Luna, R., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Martinez, E., Massey, E., Mawhiney, E., Mitchell, T., Mohabbat, K., Marinez, E., Mitchell, T., Mohabbat, K., Morjan, M., Okwuonu, G., Oragunye, N., Nickerson, E., Nwokenkwo, S., Oghh, M., Okwuonu, G., Oragunye, N., Nickerson, E., Nwokenkwo, S., Oghh, M., Okwuonu, G., Oragunye, N., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Raves, M., Rojas, A., Rojubokan, I., Rolfe, M., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Shooshtari, N., Tang, H., Shooshtari, N., Stone, H., Sutton, A., Stanley, H., Shooshtari, N., Villadon, B., Thomas, N., Tangrisa, K., Tangrisa, S., Warten, R., Washington, C., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warten, R., Washington, C., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warten, R., Washington, C., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warten, R., Washington, C., Scherer, S., Warten, R., Washington, C., Tong, R., Washing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burrehl,F., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Burkett,C., Burrell,K.L., Byrd,N.C., Chen,G., Chen,R., Cher,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,C., Chewoland,C., Cleveland,C.D., Cox,C., Chen,G., 
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HTG; HTGS_PHASE1; HTGS_DRAFT.
                                        Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R. Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Walliams, G., Williams, A., Wileczyk, R., Wooden, S., Walliams, G., Williams, A., Wileczyk, R., Wooden, S., Walliams, G., Williams, 
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Wu, Y. F.,
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Submitted (27-AUG-2000) Human Genome Sequencing of Molecular and Human Genetics, Baylor College Baylor Plaza, Houston, TX 77030, USA on Jul 31, 2001 this sequence version replaced con Jul 31, 2001 this se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Weinstock, G. and Gibbs, R. Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This sequence may represent more than one clone. NOTE: This is a 'working draft' sequence. It currently consists of 28 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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Chemistry: Dye-terminator Big Dye: 96% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 247540 bases at least Q40
Consensus quality: 264763 bases at least Q30
Consensus quality: 273200 bases at least Q30
Estimated insert size: 327546; sum-of-contigs estimation
Quality coverage: 4.1x in Q20 bases; sum-of-contigs estimation
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----- Summary Statistics
Sequencing vector: Plasmid: M77789
Sequencing vector: M13; L08821
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Oryza sativa
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* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                      AF377947.1 GI:14040068
                                                                                                                            PROGRESS ***, 5 unordered pieces AF377947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and Barrell, B.
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Sciences, Athens, Georgia 30602, USA
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                              Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 178783)
                                                                                                                                          Homo sapiens chromosome
AC068139
                                                                                                            HTG
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Cordonnier-Pratt,M.-M.
Genome Therapeutics Corporation
                  Smith, D.R
                                                                              Homo sapiens
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30935 c 30737 g 39907
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/db_xref="taxon:4530"
/chromosome="3"
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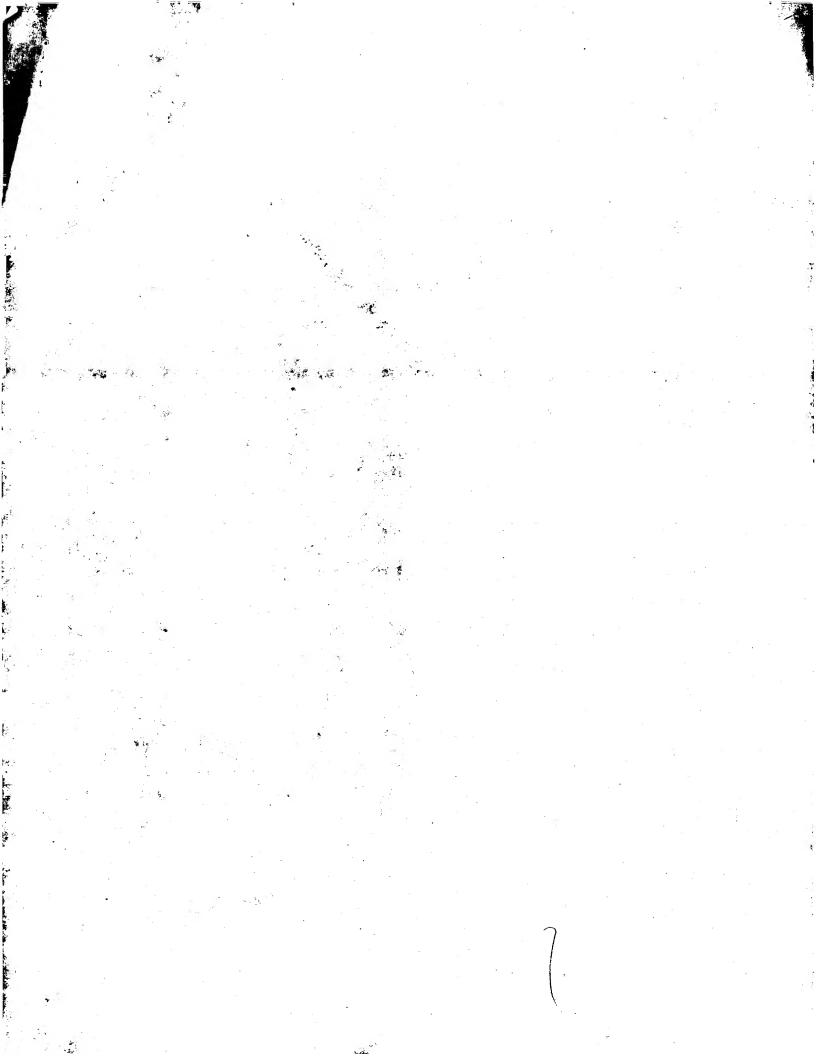
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156;
                   Submitted (18-FEB-1998) Stanford DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, 94304, USA
On Aug 12, 2000 this sequence version replaced qi:8810454.
                                                                                                                                                                                                                                                                                                            AC004153 156060 bp DNA HT Plasmodium falciparum chromosome 12 clone PROGRESS ***, 2 unordered pieces.
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Submitted (15-NOV-2000) Genome Therapeutics
Street, Waltham, MA 02453, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (29-APR-2000) Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA 02453, USA (bases 1 to 178783)
                                                                                                                                                Hyman, R.W., Fung, E.L., Qin, F., Rowley, D., Mao, J., Kurdi, O.B., Conway, A.B. and Davis, R.W. Plasmodium falciparum 3D7 chromosome 12
                                                                                                                                                                                               Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida;
1 (bases 1 to 156060)
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Direct Submission
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      12, 2000 this sequence version replaced gi:8810454 This is a 'working draft' sequence. It currently
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RESULT CNSOOEVL LOCUS DEFINITION CNSOUEVL 1101 bp DNA GSS 04-JUN-1999 Drosophila melanogaster genome survey sequence T7 end of BAC: BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit fly) GROWNER CONTROL OF THE PROPERTY OF TH

ALIGNMENTS

VERSION KEYWORDS SOURCE ACCESSION ORGANISM Drosophila GSS AL069706.1 fly), genomic survey sequence. AL069706 fruit fly.

melanogaster

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Submitted (02-JUN-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail : Genoscope.
Direct Submission Muscomorpha; Ephydro 1 (bases 1 to 1101) Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila National de Seguencage segref@genoscope.cns.fr

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BBGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo. NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's pand to Cancer individual HaC Clones the outline library and bow to Crafer individual HaC Clones the outline library. and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can found at http://bacpac.med.buffalo.edu/drosophila_bac.htm. part of a

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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                            Plasmid Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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AL106171
AL106171.1 GI:5620504
GSS.
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/clone_lib="RPCI-98"
/clone="BACR29B23"
/note="end: T7"
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/organism="Drosophila
/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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                           Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp. the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu//drosophila_bac.htm.
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Pterygota;
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scomorpha; Ephydroidea; Drosophilidae; Drosophila.
(bases 1 to 1101)
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      Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oscegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2: cn bw sp. the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at the train of the MacDAC Resource Center can be
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found at http://bacpac.med.buffalo.edu/drosophila_bac.htm
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/db_xref="taxon:727"
/clone_lib="RPCI-98"
/clone="BACR08K08"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo. NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or
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BACRI7N06 of RPCI-98 library from Drosophila melanogaster (frufly), genomic survey securocacter (frufly), genomic securocacter (frufly), 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
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Human gene number estimate provided by genome wide analysis using
                                                                                                                                                                                                                                                                                   GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                      CNS01U90 524 bp DNA GSS 12-MAY-2000
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
196C24 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  filters for hybridization from the BACPAC Resource Center can found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
Genoscope
                              Unpublished
                                               Tetraodon nigroviridis
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                                                                                                                                                                             Charaterization and repeat analysis of the compact
                                                                                                                                                                                               Weissenbach,J.
                                                                                                                                                                                                         Roest-Crollius,H., Jaillon,O., Dasilva,C.,
Bouneau,L., Billault,A., Quetier,F., Sauri
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AL167541.1 GI:7805598
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                                                                                                                                                            freshwater pufferfish
                                                                                                                                                                                                                                                            Tetraodontidae;
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                (bases 1 to
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/db_xref="taxon:7227"
/Clone_lib="RPCI-98"
/clone="BACRI7M06"
/note="end : T7"
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43.3%;
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                                                                                                                                                            Tetraodon nigroviridis
                                                DNA sequence
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                                                                                                                                                                                                                            Fizames, C.,
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Submitted (02-JUN-1999) Genoscope · Centre National de Sequencage : BP 191 91006 EVRY cedex · FRANCE (E-mail : seqref@genoscope.cns.fr · Www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and
                                                                                                                                                                                                                                                                                                          fly), ger
AL052544
                                                                                                                                                                                                            Eukaryota;
Pterygota;
                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster genome sur
BACR18L14 of RPCI-98 library from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a lar scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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erygota; Neoptera; Endopterygota; Diptera; Brachycera;
scomorpha; Ephydroidea; Drosophilidae; Drosophila.
(bases 1 to 1101)
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/note="Genoscope sequence ID : COAG196BB12SP1-end
PUC-Ori"
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/db_xref="taxon:99883"
/clone="196C24"
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43.2%;
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                                                                                                                                                                                                      Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1101)
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- Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information
                                                                                                               Submitted (02-JUN-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail :
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/note="end : T7"
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/db_xref="taxon:7227"
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Pred. No. 0.082;
'4; Mismatches 116; Indels
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                                                                                                                                        Plasmid Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 987)
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Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN12P22 of DrosBAC Library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp. the same strain used for the BDGP's pland EST libraries. A more detailed description of the library
                     Determination
                                                           Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fi
                                                                                                                         Genoscope
                                                                                                                                                                                                                                                                   GSS
                                                                                                                                                                                                                                                                                  fly), genomic survey sequence.
AL104456
AL104456.1 GI:5616067
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                                                                                                      Direct Submission
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Web : www.genoscope.cns.fr)
etermination of this BAC-end sequence was
ollaboration with the European Drosophila
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
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Determination of this BAC-end sequence was carried out as part collaboration with the Berkeley Drosophila Genome Project (BDGI The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and
                                                                                                                                                     Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequenca
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC Library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

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/plasmid = "pBeloBAC11"
/db_xref = "taxon:7227"
/clone_lib "DrosBAC"
/clone="BACN12P22"
/note = "ned : Sp6"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre
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BACN04L20 of DrosBAC library fr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library
                                                                                            Submitted (23-JUL-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail:
                                                                                                                                                                                                                                         Plasmid Drosophila melanogaster
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/clone="BACR04A23"
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/db_xref="taxon:7227"
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segref@genoscope.cns.
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d'Etude

du Polymorphisme Humain) with funding provided by a MRC

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                                                                                                                                                       Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster genome survey sequence T7 end of BAC BACNISEO4 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
                                                                                               d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha: Ephydroidea; Drosophilidae; Drosophila.
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and Genevieve I
                                                                                                                                                                                                                                                         Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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1 (bases 1 to 1200)
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
/clone_lbb="DrosBAC"
/clone="BACN04L20"
/note="end : T7"
a 62 c 2 g 2
/organism="Drosophila melanogaster"
/plasmid="pBeloBAC11"
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Contact: Genoscope
Genoscope
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1 (bases 1 to 1125)
Li,W.B., Gruber,C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
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/clone="BACN15E04"
/note="end : T7"
a 188 c 167 g
          /clone_lib="ITI_NFL006_PL2"
/clone_lib="TTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pcWVSPORT 6; Site_1: NotI; 1st strand cDNA
/note="Vector: pcWVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotIroligo(dT) primer. Five prime end
enriched with a NotIroligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcWVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DI011YB03"
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fliang@lifetech.com URL :
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                                                                                                                                                                               Human gene number estimate provided by Tetraodon nigroviridis DNA sequence
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Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic Strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                          Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org.The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of
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1: /SIDS2/gcgdata/geneseq/geneseqn/NA1980.DAT:*

2: /SIDS2/gcgdata/geneseg/geneseqn/NA1982.DAT:*

3: /SIDS2/gcgdata/geneseg/geneseqn/NA1983.DAT:*

4: /SIDS2/gcgdata/geneseg/geneseqn/NA1983.DAT:*

5: /SIDS2/gcgdata/geneseg/geneseqn/NA1985.DAT:*

6: /SIDS2/gcgdata/geneseg/geneseqn/NA1986.DAT:*

7: /SIDS2/gcgdata/geneseg/geneseqn/NA1986.DAT:*

8: /SIDS2/gcgdata/geneseg/geneseqn/NA1988.DAT:*

9: /SIDS2/gcgdata/geneseg/geneseqn/NA1989.DAT:*

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Copyright (c) 1993 - 2000 Comp
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1295.376 Million cell updates/sec
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Promoter of the be DNA encoding the boligonucleotide D1 oligonucleotide D1 oligonucleotide D2 oligonucleotide D2 oligonucleotide D2 oligonucleotide D1                                                                                                                                                                                                                                                               Description
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Human apolipoprote	AAZ31996	21	665	17.4	56.8	45	C
Human 3' apolipopr		17	605	17.4	CD.	44	a
Arachidonic acid m		21	20674	17.4	57	43	
Human chromosome 1		22	366	17.6	7	42	
Borrelia burgdorfe		20	1907	17.6	~1	41	O
cDNA encoding a SC		20	8310	17.7	7.	40	
Brassica napus FCA			9048	17.8	ω.	39	O
pNPX30 xylanase cD			2503	17.8	58.2	38	
			1132	17.8	ന	37	O
			163319	17.9	58.4	36	a
SERP gene. Plasmo			3975	17.9	æ	35	
Malaria-specific g	~		3975	17.9	58.4	34	
Borrelia burgdorfe			53585	18.0	58.8	3	a
Human chromosome 1			381	18.0	59	32	
\sim			6265	18.2	59.4	31	O
an 318013			513445	18.2	59.6	30	
B. burgdorferi ant			1410	18.4	60.2	29	C
B. burgdorferi ant			1341	18.4	60.2	28	O
Human inflammatory			700	18.5	60.4	27	a
Dictyostelium plas			5852	18.7	61	26	O
Human inflammatory			700	18.7	61	25	
Plasmodium var-7 p			19124	18.8	•	24	
Plasmodium var-7 g		18	19124	18.8	61.6	23	
Clostridium specie			6243	19.0		22	
ш	AAT4185		9789	19.3		21	
Beta glucosidase (2435	19.5	63.8	20	
Arachidonic acid m	AAC5801		20674	19.8		19	C
Nucleotide sequenc	AAA97037		2486	20.3		18	
Sequence encoding	~		4590	20.4	66.8	17	O
Oligonucleotide D1	AAF5823		244	27.8		16	C
	AAF58		244	28.0		15	
	AAF5825		938	39.7	29.	14	C
	AAF5826		936	39.7	129.8	13	O
Oligonucleotide D2	AAF58		936	39.7	29.	12	o

ALIGNMENTS

AAX60300 RESULT Clostridium beta2 toxin gene promoter and signal sequence - useful against toxins from Clostridium perfringens AAX60300 standard; DNA; Claim 1; Page 32; 46pp; French WPI; 1999-217498/19. Gibert M, Popoff MR; Clostridium perfringens Beta-2 toxin; Clostridium perfringens type C; gene promoter; vaccine; Clostridium tetani; ss. 12-AUG-1999 AAX60300; 19-SEP-1997; 19-SEP-1997; 26-MAR-1999 FR2768747-A1. Promoter of the beta-2 toxin gene of Clostridium perfringens type C. (INSP) INST PASTEUR. Ц (first entry) 97FR-0011710. 97FR-0011710. 327 ВP

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RESULT
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        Example
                            Clostridium beta2 toxin gene promoter and signal sequence against toxins from Clostridium perfringens
                                                                                           Gibert M,
                                                                                                               (INSP ) INST PASTEUR.
                                                                                                                                                                                                                         Clostridium perfringens
                                                                                                                                                                                                                                             vaccine;
                                                                                                                                                                                                                                                     Beta-2 toxin; Clostridium perfringens
                                                                                                                                                                                                                                                                            DNA encoding
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                                                           1999-217498/19
DB; AAY16591.
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        A; Page
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                                                                                                                                                                                                                                             Clostridium tetani;
                                                                                                                                                                                                                                                                                                                                           standard; DNA; 1392
                                                                                         Popoff MR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP; 141 A; 13 C;
                                                                                                                                                                                                                                                                            the beta-2 toxin of Clostridium perfringens type
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        46pp; French
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Pred. No. 2.2e-35;
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       Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses or a single surface -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence encodes the beta-2 toxin of Clostridium perfringens type C. The specification describes the Clostridium perfringens beta 2 toxin gene promoter (see AAX6030). The sequences can be used to produce vaccines against Clostridium, and especially Clostridium perfringens, or Clostridium
                                                                                                               26-JUL-1999;
17-MAR-2000;
                                                                                                                                                                     01-FEB-2001.
                                                                                                                                                                                                                                  gene expression;
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  Nucleic acids containing electron-transfer group, useful as labels hybridization assays, e.g. for genotyping, allowing repeat analyses
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                    WPI; 2001-159728/16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface
 Umek RM;
                    (CLIN-) CLINICAL MICRO SENSORS
                                          26-JUL-1999;
17-MAR-2000;
                                                                            26-JUL-2000;
                                                                                                  01-FEB-2001
                                                                                                                        WO200107665-A2
                                                                                                                                                                   gene
                                                                                                                                                                             Electron-transfer group;
                                                                                                                                                                                                   Oligonucleotide D2004
                                                                                                                                                                                                                        24-APR-2001
                                                                                                                                                                                                                                               AAF58259
                                                                                                                                                                                                                                                                    AAF58259 standard; DNA; 936 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                          436
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                                                                                                                                                                                                                                                                                         6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present invention relates to a composition comprising
                                                                                                                                                                                                                                                                                                                          wwwwwwwwwwwwwwww 462
                                                                                                                                                                                                                                                                                                                                                                                                                                      aaaagtgtaaaaataattatttttattttaaatttgttaaaaatttgatataattgaattg 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aaagtgttctcgggggacacttttttgttttaaaaaggaaaatataaaatataaatttagat 180
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                                                                                                                                                                                                                                                                                                                                              tttatgttttcatgttttcttattgtt 327
                                                                                                                                                                  expression;
                                                                                                                                                                                                                                                                                                                                                                                         taaaaaaaatttcagggggaatataaatgaaaaaaattatttcaaagtttactgtaatt 300
                                                                                                                                                                                                                                                                                                                                                                                                                  h 39.8%;
Similarity 0.9%;
3; Conservative 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Page 127; 159pp; English.
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                                           99US-0145695.
2000US-0190259.
                                                                            2000WO-US20476
                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                              ETM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 9.2e
68; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 130.2;
                                                                                                                                                                            mismatch; genotyping;
                     INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ,.2e-10;
56;
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RESULT
AAF58262
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids containing electron-transfer group, useful as labels hybridization assays, e.g. for genotyping, allowing repeat analyses a single surface \,
                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                 Electron-transfer group; ETM; mismatch;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide D2007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-159728/16
                                                                        26-JUL-1999; 99US-0145695.
17-MAR-2000; 2000US-0190259.
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                                                                                                                                                                                                                                                                 WO200107665-A2
                                                                                                                                                                                                                                                                                                                                                                           gene expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-APR-2001
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                   (CLIN-) CLINICAL MICRO SENSORS
                                                                                                                                                       26-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         436
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nes 3; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative 268; Mismatches
                                                                                                                                                       2000WO-US20476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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0.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВP
                                                                                                                                                                                                                                                                                                                                                                                                    genotyping;
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                                                                                                               Synthetic
                                                                                                                                                                     Oligonucleotide D1876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface \,
           26-JUL-1999; 99US-0145695
17-MAR-2000; 2000US-0190259
                                          26-JUL-2000; 2000WO-US20476.
                                                                                         WO200107665-A2
                                                                                                                                               Electron-transfer group;
                                                                                                                                                                                            24-APR-2001 (first entry)
                                                                                                                                                                                                                   AAF58255;
                                                                                                                                                                                                                                          AAF58255 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 936 BP; 5 A; 139 C; 10 G; 6 T; 776 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention
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Local Similarity 0.9%; Pred. No. 9.2e
nes 3; Conservative 268; Mismatches
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                                                                                                                                   expression;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    relates to a composition comprising
                                                                                                                                                                                                                                          938
                                                                                                                                              ETM; mismatch; genotyping;
                                                                                                                                                                                                                                          ВP
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7.2e-10;
56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22; Length
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RESULT 9
AAF58252/c
ID AAF582
PR XXX
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Best Local Similarity
"-+-hes 3; Conserv
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                                                                                                                  Electron-transfer group; gene expression; ss.
                                                                                                                                                     Oligonucleotide D1835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatch and single-nucleotide polymorphisms, e.g. for genotyping,
                      26-JUL-2000; 2000WO-US20476
                                              01-FEB-2001.
                                                                     WO200107665-A2
                                                                                             Synthetic
                                                                                                                                                                                                     AAF58252;
                                                                                                                                                                                                                            AAF58252 standard;
                                                                                                                                                                              24-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           monitoring gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-159728/16
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                                                                                                                                                                                                                                                                                       436 WWWWWWWWWWWWWWWWWWWW 462
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                                                                                                                                                                                                                                                                                                                                                                                     39.8%; Score 130.2; DB ilarity 0.9%; Pred. No. 9.2e-10; Conservative 268; Mismatches
                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                             DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       relates to a composition comprising
                                                                                                                                                                                                                             936
                                                                                                                              ETM; mismatch;
                                                                                                                                                                                                                            ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      776 other;
                                                                                                                              genotyping;
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for genotyping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22;
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26-JUL-1999;

99US-0145695

2000US-0190259

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RESULT 10
AAF58254/c
ID AAF58254 standard;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Umek
                 26-JUL-2000; 2000WO-US20476
                                      01-FEB-2001
                                                                             Synthetic
                                                                                               gene expression; ss
                                                                                                         Electron-transfer group; ETM; mismatch; genotyping;
                                                                                                                            Oligonucleotide D1875
                                                                                                                                               24-APR-2001
                                                                                                                                                                   AAF58254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 936 BP; 4 A; 139 C; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 6; Page 127; 159pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a single surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids containing electron-transfer hybridization assays, e.g. for genotyping,
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                                                                                                                                                                                      DNA;
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                                                             gene expression;
                                                                        Electron-transfer
                                                                                            Oligonucleotide D1954.
                                                                                                                                      AAF58257;
                                                                                                                                                          AAF58257 standard; DNA;
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17-MAR-2000;
                                         Synthetic
                                                                                                                  24-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     conservative
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2000US-0190259
                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   containing electron-transfer group, useful as labels in assays, e.g. for genotyping, allowing repeat analyses on
                                                               SS
                                                                        group;
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                                                                                                                                                           936
                                                                         ETM;
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269; Mismatches
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                                                                         mismatch;
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                                                                        genotyping;
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01-FEB-2001.

WO200107665-A2

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WO200107665-A2
                  Synthetic
                                    gene expression;
                                              Electron-transfer
                                                                Oligonucleotide D2004
                                                                                  24-APR-2001
                                                                                                    AAF58259;
                                                                                                                      AAF58259 standard; DNA; 936
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a single surface
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Umek RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CLIN-) CLINICAL MICRO SENSORS
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17-MAR-2000;
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2; Conserv
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                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                               BP;
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2000US-0190259
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                                                                                                                                                                                                                                                                                                                                                                                                                                              5 A;
                                      SS
                                              group;
                                                                                                                                                                                                                                                                                                                                                                                                         39.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                              142 C; 7 G; 6 T; 776 other;
                                              ETM;
                                                                                                                                                                                                                                                                                                                                                                                                 269;
                                                                                                                                                                                                                                                                                                                                                                                               ; Score 129.8; DI
Pred. No. 1e-09;
269; Mismatches
                                                                                                                      ВР
                                              mismatch;
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                                             genotyping;
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Matches 2
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                        gene expression;
                                    Electron-transfer group;
                                                              Oligonucleotide D2007
                                                                                                              AAF58262;
                                                                                                                                      AAF58262 standard; DNA;
                                                                                      24-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses or a single surface
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 936 BP; 6 A; 138 C; 8 G; 8 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             monitoring gene expression.
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17-MAR-2000; 2000US-0190259.
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                                                                                      (first entry)
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                                       ETM; mismatch;
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Pred. No. 1e-09;
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                                     genotyping;
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gene expression; ss
          Electron-transfer group; ETM;
                                Oligonucleotide D1876
                                                        24-APR-2001
                                                                                                    AAF58255
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17-MAR-2000;
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           mismatch;
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          genotyping;
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                                                                              AAF58238 standard; DNA; 244 BP
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17-MAR-2000;
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Oligonucleotide D1250:D1102 24-APR-2001 (first entry)

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Search completed: January 24, 2002, 02:22:17 Job time: 1885 sec
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                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping, monitoring gene expression.
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                                                                                                                                                                                                                                                                                                                                                                                 Sequence 244 BP; 19 A; 9 C; 12 G; 10 T; 194 other;
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17-MAR-2000; 2000US-0190259.
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                                                                                     102 aagtatagttaataaataaaagtgttctcgggggacacttttttgttttaaaaaggaaa 161
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6	15	4.6	50	11	C01094	C01094 HUMGS000775
7	14	4.3	24	13	AZ781748	AZ781748 2M0021M18
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ALIGNMENTS

	FEATURES source		JOURNAL COMMENT	REFERENCE AUTHORS TITLE	ORGANISM	ACCESSION VERSION KEYWORDS SOURCE	RESULT 1 AU011968 LOCUS DEFINITION
/Strain="972" /Strain="972" /db_xref="taxon:4896" /clone="spc06162" /clone_lib="Schizosaccharomyces pombe late log phase cDNA" /clone_lib="Schizosaccharomyces pombe was prepared by cloning cDNA into the Smal site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of	Location/Qualifiers 142 /oran is m "Schiopsopharomicos pombo"	Genome Research Group National Institute of Radiological Sciences 9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan Email: morimyo@nirs.go.jp.	Dombe Dombe Unpublished (1998) Contact: Mitsweet Norimyo	1 (bases 1 to 42) 1 (bases 1 to 42) Morimyo,M. and Mita,K. Identification of expressed sequence tags of Schizosaccharomyces	Schizosaccharomyces pombe Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces	AU011968 AU011968.1 GI:3356877 EST. fission yeast.	AU011968 42 bp mRNA EST 03-AUG-1998 AU011968 Schizosaccharomyces pombe late log phase cDNA Schizosaccharomyces pombe cDNA clone spc06162, mRNA sequence.

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JOURNAL
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            AU011971 42 bp mRNA EST 03-AUG-1998
AU011971 Schizosaccharomyces pombe late log phase cDNA
Schizosaccharomyces pombe cDNA clone spc06165, mRNA sequence.
AU011971
AU011971.1 GI:3356880
EST.
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National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Mitsuoki Morimyo
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1998)
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1: morimyo@nirs.go.jp.
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/clone="spc06163"
/clone_11b="Schizosaccharomyces pombe late log
/cone_11b="Schizosaccharomyces pombe late log
/sex="h minus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="972"
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9.6e+04;
hes 0;
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9.6e+04;
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AU011973 Schizosaccharomyces pombe late
Schizosaccharomyces pombe cDNA clone spc
AU011973
                                                                                                                   Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba
Email: morinyo@nirs.go.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity 100
15; Conservative
                                                                                                                                                                                                        Unpublished (1998)
Contact: Mitsuoki Morimyo
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Morimyo, M. and Mita, K.
Identification of expressed sequence
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National Institute of Radiological Sciences
National Institute of Radiological Sciences
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                                                                                                                                                                                                                                                                                                                                                                                 fission yeast
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 42)
Morimyo, M. and Mita, K.
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1: morimyo@nirs.go.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: M13mp19; The cDNA library of Schizosaccharomyces pombe was prepared by clining cDNA into the Smal site of M13mp19 DNA and the direction of DNA sequences was not always from 5′ to 3′. The cDNA data of schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)" a 1 c 7 g 15 t
/organism="Schizosaccharomyces pystrain="972"
/db_xref="taxon:4896"
/clone="spc06167"
/clone_lib="Schizosaccharomyces
/sex="h minus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:4896"
/clone="spc06165"
/clone_lib="Schizosaccharomyces pombe late log phase cDNA"
/sex="h minus"
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/strain="972"
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                                                                                                                                                        Chiba, Chiba
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236 aattgtaaaaaaaat 250
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similar to
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA Library Preparation: Stratagene, Inc. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: John Ensley, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA922891
                                                                                                                                                                                                                                                                                                                                                                                                                                                               www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
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1 c 7 g 15 t
                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1486233"
/clone_lib="NCI_CGAP_HN3"
                                                                                                                                                                                                                                                      /tissue_type="squamous cell carcinoma from base of tongue"
/lab_host="SOLR (kanamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eutheria; Primates;
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                                                                 DB 10; I
. 9.1e+04;
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1 Similarity 100.0%;
15; Conservation
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2M0021M18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0021M18 F, DNA sequence.
A2781748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1-3, Yanada-oka, Suita, Osaka Pref. 565, Japan
Tel: 06-877-5111(ex.3315)
Email: kousaku@imcb.osaka-u.ac.jp
Human Gene Signature, 3'-directed cDNA sequence. We are not
submitting the same cDNA sequence redundantly to DDBJ since 1993.
For the abundance information of clones with this sequence in this
library and as well as in other 3'-directed libraries, see '
http://www.imcb.osaka-u.ac.jp/bodymap'. The sequences of the clones
represented by this GS sequences is also found there.
Contact: Robert B. Weiss
University of Utah Genome
University of Utah
                                                                                                   Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Du
Islam, H., Longacre, S., Mahmoud, M., Meenen, E.,
M., Rose, M., Rose, R., Stokes, R., Tingey, A.,
and Wright, D., Weiss, R.
                                                                                                                                                   1 (bases 1 to 24)
Dunn, D., Aoyagi, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BodyMap; human gene expression database Unpublished (1995)
Contact: Okubo,K
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Mammalia; Eutheria;
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                                                     Unpublished (2000)
                                                                   plasmid inserts
                                                                                     Mouse whole genome
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/dev_stage="adult"
6 c 5 g 15 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                   scaffolding with
                                                                                                                                                                                      Chordata;
Rodentia;
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Pred. No.
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                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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9e+04;
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Meenen,E., von Niederhausern,A.
                                                                                   paired
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Best Local
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           Osaka University
1-3, Yamada-oka, Suita, Osaka Pref. 565, Japan
Tel: 06-877-5111(ex.3315)
                                                                                                          BodyMap; human gene expression database Unpublished (1995)
Contact: Okubo,K.
                                                                                          Institute for Molecular and Cellular Biol
                                                                                                                                                                                    Okubo, K.
                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                           EST.
                                                                                                                                                                                                                                                                                                                                           sequence.
C01204
C01204.1 GI:1433434
                                                                                                                                                                                                                                                                                                                                                                                                             HUMGS0007904 Human adult (K.Okubo) Homo sapiens cDNA, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                          C01204
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1 (bases 1 to 28)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plate: 0021 row: M column: 18 Seq primer: CGTTGTAAAACGACGGCCAGT
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Err
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWNA2 (gil4732114 jgh) AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
kousaku@imcb.osaka-u.ac.jp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
/clone="UUGC2M0021M18"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="Male"
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/strain="C57BL/6J"
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, 2.9e+05;
thes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AU038857 34 bp mRNA EST 29-MAR-1999
AU038857 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium
discoideum cDNA clone SSL566, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                      3-3-10 Ten nodai, Tsukuba, Ibaraki 305, Japan
Email: d402hu@sakura.cc.tsukuba.ac.jp
PROJECT = 'Dictyostelium discoideum cDNA project in Japan'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dictyostelium discoideum Dictyostelium discoideum
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                                                                                                                                                                                                                                                                                                                                                                                                               University of Tsukuba
                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Hideko Urushihara
Institute of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99156227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Res. 5 (6), 335-340 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             development
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1 (bases 1 to 34)
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Location/Qualifiers
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/db_xref="taxon:9606"
/clone_lib="Human adult (K.Okubo)"
/dev_stage="adult"
3 c 3 g 10 t 1
                                                                                                                                                                                  /clone_lib="Dictyostelium discoideum /dev_stage="slug" 0 c 0 g 11 t
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/clone="SSL566"
                                                                                                                                                                                                                                                                                    /strain="AX4"
                                                                                                                                                                                                                                                                                               /organism="Dictyostelium
                                                                                        4.3%;
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                                                                      Score 14; DB; Pred. No. 2.5
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2.5e+05;
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2.7e+05;
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                                                                                                                                 sequence.
AW333885
AW333885.1
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14; Conserv
                     University of Utah Genome Center University of Utah
                                                                                   plasmid inserts
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                  clone UUGC1M0490C17 R, DNA sequence. AZ634761
                                                                                                                                                                                                                                                                                                                                                                                                                      1M0490C17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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S27E6 AGS-1 Pneumocystis
                                                                 Contact: Robert B.
                                                                                                                          Mouse whole genome scaffolding with paired
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 Morgan Building, University of Kentucky, Lexington, KY 40506-0225, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      School of Biological Sciences University of Kentucky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2000)
Contact: Staben C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smulian,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C., Edman,J.C., Kovacs,J. and Cushion,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pneumocystidaceae; Pneumocystis.
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Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="E. coli"
/note="Vector: Lambda ZAP II; Site_1: EcoRI; Site_2: XhoI;
/note="Vector: Lambda ZAP II; Site_1: EcoRI; Site_2: XhoI;
P. carinii organisms (3x10e9) from a single rat (99-1-6,
P. carificed on 3/17/99) at Cincinnati VA facilities.
Trizol extracted RNA. Oligo dT priming, standard
conditions described by vendor, Stratagene. Further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        details see www.uky.edu/Project/Pneumocystis/'
0 c     6 g     17 t
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/db_xref="taxon:38081"
/clone_lib="A6S-1"
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100.0%; Pr
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Pred. No.
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2.4e+05;
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                                                                                                                        Islam,H., Longacre,S., Mahmoud,M., Meenen,E.,
,M., Rose,M., Rose,R., Stokes,R., Tingey,A.,
and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                     AZ459612 46 bp DNA GSS 04-OCT-2000 1M0264002R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0264002 R, DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                    Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
                                                                                                                                                                                                         Mammalia; Eutheria;
1 (bases 1 to 46)
                                                                                                                                                                                                                                                                       Mus musculus
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Location/Qualifiers
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Email: ddunn@genetics.utah.edu
Email: 0.000 Std Error: 0.
University of Utah Genome Center 
University of Utah
                                       Contact: Robert B.
                                                             Unpublished (2000)
                                                                                   plasmid inserts
                                                                                                       Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732141 gbln4F129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E, coll XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
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/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Mouse 10kb plasmid UUGC1M library"
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/strain="C57BL/6J"
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Pred. No.
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2.4e+05;
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Contact: Robert B. Weiss
University of Utah Genome Center
                                                                      plasmid inserts
                                                                                                                 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                 AZ345468 47 bp DNA GSS 29-SEP-2000 1M0080N12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic Clone UUGC1M0080N12 F, DNA sequence.
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                                                                                         Mouse whole genome scaffolding with paired end reads from 10kb
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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AZ345468.1 GI:10424705
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Insert Length: 10000 Std Error: 0.00
Plate: 0264 row: O column: 02
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (9i|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli xL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/note="Vector: PW042nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0264002"
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: I.M.A.G.E. Consortium, LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                            BE043289 50 bp mRNA bs: hk49d05.y1 NCI_CGAP_Ov34 Homo sapiens cDNA clone IMAGE:3000009
                                                                                                                                                                                                                                                                                                                                                                                                 mRNA sequence.
BE043289
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                                                                                                                                   Tumor Gene Index
                                                                                                                                                        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                       BE043289.1 GI:8360342
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Insert Length: 10000 Std Erro
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                         human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory Mouse DNA Resource
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/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="Male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Mouse 10kb plasmid UUGC1M library"
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2.3e+05;
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                                                                                                                                                                                                                  Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14;
                                                                                                                                  Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
Project Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
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T. brucei sheared genomic
                                                                                                                                                                                                                                                                                                                                                                                                      Constructed at the Institute for Genomic Research (TIGR),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trypanosoma brucei.
Trypanosoma brucei
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                                                                                                                                                                                                                                                                                                                                                                                                                                  nhl@sanger.ac.uk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              borderline ovarian carcinoma, cDNA made by oligo-dT priming. Directionally cloned. Size-selected on agarose gel, average insert size 500 bp. Primary library, non-amplified. "
                       /organism="Trypanosoma
/strain="TREU927"
/db_xref="taxon:5691"
/clone="154f10"
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/note="Organ: ovary; Vector: pAMP1; mRNA made from
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/clone_lib="NCI_CGAP_Ov34"
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tive 0; Mismatc
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2.2e+05;
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Insert Length: 10000 Std Erro
Plate: 0059 row: M column: 12
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1M0059M12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AZ331628.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 19)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            308,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 quality sequence stop: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                             (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was punified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114 [gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and the control of the charced managements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                     adaptored vector DNA, a chemically-competent E.
and selected
                                                                 purified.
                                                                                                                                                                                                                                                                                                                                                        Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                  musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
/clone="UUGC1M0059M12"
                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
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100.0%;
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                                                               The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Weiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polymers Research Bldg.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 14;
Pred. No.
for ampicillin
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         and transformed into
E. coli XL10-Gold (Stratagene) cells
cillin resistance "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 13;
. 2.2e+05;
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RESULT 17
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ORGANISM
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 AAATAAAATTTAG 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0107 row: I column: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plate: 0107 row: I column: 24
Seg primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 801 585 5606 Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 25)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2M0107124F mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0107124 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AZ829725.1 GI:12999549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 308,
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ilarity 100.0%;
Conservative (
was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi14732114|gb|AF1291072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                                                    musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="UUGC2M0107I24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="Male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Std Error:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 S.
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nes 13; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AZ309204 26 bp DNA GSS 29-SEP-2000 LM0013F07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0013 row: F column: 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Class: plasmid ends
High quality sequence stop: 26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plasmid inserts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                     (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative aparose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi14732114|gb|AF1129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complements vector has insert adaptors.
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       with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jack
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                                                                                                                                                                                                                                                                                                                                                      Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0013F07"
                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0177 row: A column: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AZ866662 26 bp DNA GSS 2M0177A18F Mouse 10kb plasmid UUGCIM library clone UUGC2M0177A18 F, DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     University of Utah Genome Center University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
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was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pNA22 (gil4732114)phAF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
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/note="Vector: PWD42nv; Purified genomic DNA from M.
/notesulus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DI
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                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0177A18"
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AZ784620 27 bp DNA GSS 2M0027P04R Mouse 10kb plasmid UUGC1M library clone UUGC2M0027P04 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucel (PREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
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T. brucei sheared genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Details of T. brucei sequencing at the Sanger Centre are at http://www.sanger.ac.uk/Projects/T_brucei/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: nelsayed@tigr.org
Details of T. brucei sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Constructed at the Institute for Genomic Research (TIGR),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nhl@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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Larity 100.0%;
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/strain="TREU927"
/db_xref="taxon:5691"
/clone="123b12"
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LOCUS AZ452653 28 bp DNA GSS 04-OCT-2000 DEFINITION 1M0252E07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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University of Utah
University of Utah
Rm. 308, Biomedical Polymers Reso
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Fax: 801 585 7177
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/clone="UUGC2M0027P04"
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/strain="C57BL/6J"
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Location/Qualifiers
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Fax: 801 585 7177
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University of Utah
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/sex="Male"
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RESULT
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                      24
                                                                            TTATTTTAAATTT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0461 row: C column: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1m0461C19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1m0461C19 R, DNA sequence. AZ623794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 30.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dunn, D., Aoyagi, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                         10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                       was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="UUGC1M0461C19"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
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/strain="C57BL/6J"
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                                                                                                                                                    Beacorn, T., Duval, B., Hamil, C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
Insert Size: 674
High quality sequence starts: 1
High quality sequence stops: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
The WashU-Merck EST Project
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1 (bases 1 to 32)

Hillier, L. Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman W. Clark, M., Tonoca C. Marzon M. Control T. Cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H40874 32 bp mRNA 31-JUL-1995
yn97e10.s1 Soares adult brain N2b5HB55Y Home sapiens cDNA clone
IMAGE:176394 3' similar to gb:x54150_rnal IMMUNOGLOBULIN ALPHA FC
RECEPTOR PRECURSOR (HUMAN);, mRNA sequence
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Location/Qualifiers
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Fax: 314 286 1810
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1 0 c 0 g 26 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pm773 vector (Pharmacia). Library went through one round of normalization to a Cot = 53. Library constructed by Bento Soares and M.Fatima Bonaldo. The adult brain RNA was provided by Dr. Donald H. Gilden. Tissue was acquired 17-18 hours after death which occurred in consequence of a construction of the consequence of a cons
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/clone="IMAGE:176394"
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4.0%; Score 13; DB 11;
100.0%; Pred. No. 6.4e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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Location/Qualifiers
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Fax: 801 585 7177
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                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
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                                                                                                                                                                                                                                                                                   purified. The sheared, auaptored into adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

a 5 c 4 g 19 t
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/clone="UUGC1M0263E04"
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/strain="C57BL/6J"
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                                                                        100.08; F1
                                                                                                                          Score 13; DB 13;
Pred. No. 6.4e+0
                                                                                     6.4e+05;
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                     JUDY 34 bp DNA GSS 1M0392K72R Mouse 10kb plasmid UUGCIM library Mus clone UUGCIM0392K22 R, DNA sequence. Az586746 Az586746.1 GI:1170Raare
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34 bp mRNA

ok73c02.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1519586
similar to SW:UFD1_HUWAN 092890 UBIQUITIN FUSION DEGRADATION
PROTEIN 1 HOMOLOG;, mRNA sequence.
house mouse
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Location/Qualifiers
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 34)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/clone="IMAGE:1519586"
/clone_lib="NCI_CGAP_GC4"
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/lab_host="DH10B"
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100.0%; Pred. No..6;
tive 0; Mismatches
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                                               AZ781725 34 bp DNA GSS LD-FEB-ZUUL 2M0021114F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0021114 F, DNA sequence.
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0392 row: K column: 22
                     AZ781725
AZ781725.1 GI:12914706
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Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and Wright, D., Weiss, R.
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M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pubMad (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and contribute of the complementary to the insert adaptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                       purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0392K22"
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Best Local Similarity
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mRNA sequence.
AW246486
AW246486.1 GI:6589479
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2821545.3prime NIH_MGC_7
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Insert Length: 10000 Std Error:
Plate: 0021 row: I column: 14
Seq primer: CGTTGTAAAACGACGGCCAGT
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1 (bases 1 to 34)
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/clone="UUGC2M0021I14"
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/strain="C57BL/6J"
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Pred. No. 6.2e+05;
                                                                                                                      mRNA
                                                                                           Homo sapiens cDNA clone IMAGE: 2821545 3',
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nes 13; Conserv
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Email: cgapbs r@mail.nih.gov

Tissue procurement: DCTD/DTp cDNA Library Preparation: Ling

Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.

Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing

project Clone distribution: MGC clone distribution information can

be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality

Scores: PHRED from University of Washingtion Genome Center:

PHRAP suite. Poly-T Identification: patkMatch.pl from Berkeley

Drosophila Genome Project. University of Washingtion Genome Center:

http://www.genome.washington.edu Low Quality Sequence: 35

contiguous PHRED high quality bases following vector sequence. Very

peaks following vector sequence. Polyadenylation: Based upon the

presence of a XhoI site followed by a run of 14 or more T residues

at the beginning of the sequence of the county income.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                 Homo sapiens
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                                                                                                                        D45807.1 GI:662761
                                                                                                                                            D45807
                                                                                                                                                                          HUMGS03025 Human adult lung 3' directed 3', mRNA segmence
                                                                                                                                                                                                                   D45807
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
Other_ESTs: 2821545.5prime
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National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="DH10B (phage-resistant)"
/note="organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: RCGRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:2821545"
/clone_lib="NIH_MGC_7"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                   35 bp
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Pred. No.
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6.2e+05;
thes 0;
                                                                                                                                                                                           MboI cDNA
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                                                                                                                                                                                        Homo sapiens cDNA
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ORGANISM
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AZ314238
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 35)
Itoh,K., Okubo,K., Yosii,J., Yokouchi,H. and Matsubara,K. An expression profile of active genes in human lung
DNA Research 1, 279-287 (1994)
95336275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0030 row: N column: 24
Seg primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                     University of Utah Genome Center University of Utah
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                                                                                                                                                                        High quality sequence stop: 36.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                            Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria;
1 (bases 1 to 36)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
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Tel: 06-877-5111 x3910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Kohichi Itoh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Institute for Molecular and Cellular Biology
                                                                                                                                                                                                               lass: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                 Biomedical Polymers Research Bldg.,
                                       /sex="Male"
                                                                             /db_xref="taxon:10090"
/clone="UUGC1M0030N24"
                                                                                                            /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Human adult lung 3' directed MboI cDNA"
/note="Adult human lung, 3' directed MboI"
3 c 5 g 13 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
                   /lab_host="E. Coli strain XL10-Gold, T1-resistant,
                                                         /clone_lib="Mouse 10kb plasmid UUGC1M library"
   /note="Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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PWD42nv; Purified genomic DNA from M.
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6.2e+05;
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                                                                                                                                                                                                                                               High
                                                                                                                                                                                                                                                                                                                                                              CDNA Library Preparation: Stratagene, Inc. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                   Trace considered overall poor quality Seq primer: -40ml3 fwd. ET from Amers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        National Cancer Institute / National Institute of Dental Research, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                         www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tissue Procurement: John Ensley, M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCI/NIDR-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA913140.1 GI:3052532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA913140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MDH1-VMA5 INTERGENIC REGION. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immen
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                                                                                                                                                                                                                                               quality sequence stop: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cgapbs-r@mail.nih.
/tissue_type="squamous cell carcinoma"
/lab_host="SQLR (kanamycin resistant)
/note="Organ: lymph node; Vector: Bluescript SK-; Site_1:
ECORI; Site_2: XhoI; Cloned unidirectionally. Primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (http://www.jax.org/fesources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA
                                                                                               /clone="IMAGE:1483067"
/clone_lib="NCI_CGAP_HN1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                         information can be
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REFERENCE AUTHORS

COMMENT

JOURNAL TITLE

FEATURES

source

ACCESSION VERSION

SOURCE KEYWORDS

ORGANISM

RESULT 3 AA913140

DEFINITION LOCUS Вb Š

Matches Query Match

Local

BASE COUNT

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Best Local Similarity
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                                                                                                                                                                                  '110 ttaataaataaaa
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AA916625 40 bp mRNA EST 10-JUN-1998 om05g12.sl Soares_NFL_T_GBC_Sl Homo sapiens cDNA clone TWAGE:1540198 3' similar to SW:NU5M_TRYBB P04540 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 ;, mRNA sequence.
                                                                                                                                                                                                                     13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: morimyo@nirs.go.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1998)
Contact: Mitsuoki Morimyo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 37)
Morimyo,M. and Mita,K.
Identification of expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomyco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:4896"
/clone="spc04510"
/clone_lib="Schizosaccharomyces pombe late log
/sex="h minus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="972"
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                                                                                                                                                                                                                                                                                                                   AA922076 40 bp mRNA EST 21-APR-1998 oh08g07.sl NCI_CGAP_CO8 Homo Sapiens cDNA clone IMAGE:1457244 similar to TR:Q34096 Q34096 MUREZ PROTEIN. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov

Email: cgapbs-r@mail.nih.gov

This clone is available royalty-free through LLNL; contact the

TMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Trace considered overall poor quality

Insert Length: 1026 Std Error: 0.00

Insert Length: 1026 Std Error: O.00
                    Tissue Procurement: Christopher Moskaluk, M.D., Emmert-Buck, M.D., Ph.D.
                                                             Email:
                                                                             Contact: Robert Strausberg, Ph.D
                                                                                                  Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 40)
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Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
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                                                                                                                                       National Cancer Institute, Cancer
                                                                                                                                                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
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  cDNA Library Preparation: M. Bento Soares, Ph.D.
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                                                           cgapbs-remail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:1540198"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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Pred. No.
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                                                                                                                                         Genome Anatomy Project (CGAP),
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BodyMap; human gene expression database Unpublished (1995)
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                                                                                                                                                                                                     submitting the same CDNA sequence redundantly to DDBJ since 1993. For the abundance information of clones with this sequence in this library and as well as in other 3'-directed libraries, see 'http://www.imcb.osaka-u.ac.jp/bodymap'. The sequences of the clones
                                                                                                                                                                                                                                                                                                          1-3,Yamada-oka, Suita, Osaka Pref. 565, Japan
Tel: 06-877-5111(ex.3315)
Email: kousaku@imcb.osaka u.ac.jp
Human Gene Signature, 3'-directed cDNA sequence. We are not
                                                                                                                                                                                                                                                                                                                                                                                                              Institute for Molecular and Cellular Biol Osaka University
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                                                                                                                                                   represented by this GS sequences is also found there.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Okubo, K.
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Mammalia; Eutheria;
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DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/lab_host="DH10B"
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/clone_lib="NCI_CGAP_Co8"
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100.0%; Pr
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0; Mismatches
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5.9e+05;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plate: 0011 row: M column: 12 Seq primer: CGTTGTAAAACGACGGCCAGT Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AZ777050 41 bp DNA GSS 16-FEB-2001 2M0011M12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0011M12 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 41.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
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ilarity 100.0%;
Conservative
was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA
                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                            Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
/clone="UUGC2M0011M12"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
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5.8e+05;
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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 AAAAGATATATTA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 801 585 5606
Fax: 801 585 7177
Email: 801 64 7177
Email: 801 64 777
Email: 801 64 777
Email: 801 64 777
Email: 801 585 7177
Flate: 801 585 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AZ371136 43 bp DNA GSS 02-OCT-: 1M0122N05F Mouse 10kb plasmid UUGC1M library Mus musculus clone UUGC1M0122N05 F, DNA sequence.
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Islam, H., Longacre, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 43.
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1 (bases 1 to 43)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                     was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pNDA2 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and
adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells
                                   purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
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/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="UUGC1M0122N05"
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University of Utah
Rm. 308, Biomedical Polymers Reso
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Contact: Robert B.
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Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
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          (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pDM42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared adaptored mouse DNA was annealed to
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Length: 10000 Std Error: 0.00
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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a 2 c 2 g 11 t
adaptored vector DNA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: henkelg@aurorabio.com

pools of cells were isolated from a GenomeScreen(TM) library. The
library of cells was generated by retroviral integration of a gene
tagging element consisting of: 1) A promoterless beta-lactamase
proceeded by a splice acceptor as a reporter for gene expression;
2) A promoter driving neomycin resistance followed by a splice
donor to trap downstream exons. 3' RACE from neomycin gene was
performed using total RNA from isolated pools. Output was shotgun
cloned in pAmp-1 and used to transform DH5-alpha competent
bacteria. 5' ends of reported sequences were immediately preceded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     by splice donor from the trapping construct. Class: exon-trapped.
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sapien.
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Aurora Biosciences Corp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Henkel,G., Liyanage,M., F., Durick,K. and Pollok,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 8584046719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 8584048436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Exon-trap tags from a T47D GenomeScreen(TM) Library
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a 7 c 8 g 22 t
                                                                                                                                                                                                                       /note="Organ: Breast; Vector: pAmp-1; 3' RACE of from genetrap pools; shotgun clone in pAmp-1 and transform DH5-alpha competent bacteria."

9 c 5 g 11 t
                                                                                                                                                                                                                                                                                                                    /clone_lib="Genetrap T47D Human Breast Carcinoma Library"
/tlssue_type="Carcinoma"
/cell_type="Epithelial"
/cell_line="T47D"
                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
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D20668.1
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3-1 Yamada-oka, Suita, Osaka 565, Japan.
Location/Qualifiers
                                                                    Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Okubo,K., Fukushima,A., Yoshii,J., Niiyama,T., Yoshinari,H., Arimoto,J. and Matsubara,K. Institute for Molecular and Cellular Biology
                                                                                                                                                                                            Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 46)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Okubo,K., Fukushima,A., Yoshii,J., Niiyama,T., Kojima,Y., Yoshinari,H., Arimoto,J. and Matsubara,K.
                                                                                                                                                            Mouse whole genome scaffolding with paired end reads
                                                                                                                                                                                 and Wright, D., Weiss, R.
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Mammalia; Eutheria;
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/clone_lib="Human promyelocyte"
/note="Female, adult, cell_line = HL60, cell_type
promyelocyte. "
6 c 6 g 14 t 2 others
                                                   Biomedical Polymers Research Bldg.,
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/db_xref="taxon:9606"
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Mus musculus
Eukaryota; Metazoa; Chordata;
Eukaryota; Metazoa; Rodentia;
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                                                               Contact: Robert B. University of Utah University of Utah
                                                                                                                                                                              Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D.,Weiss,R.
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Insert Length: 10000 Std Error: (
Plate: 0264 row: O column: 02
Seg primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                              Mammalia; Eutheria;
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                                            Rm. 308,
                                                                                                                            Unpublished (2000)
                                                                                                                                          plasmid inserts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWA2 (gil4732114)gb|AFT290721), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        585 5606
                                              Biomedical
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory Mouse DNA Resource
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/clone="UUGC1M0264002"
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                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 46)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly, M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
               University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Res
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AZ991460 46 bp DNA GSS 27-APR-2001
2M0275K07R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0275K07 R, DNA sequence.
                                                                                               Contact: Robert B.
                                                                                                                   Unpublished (2000)
                                                                                                                                                               Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                             AZ991460
AZ991460.1 GI:13862687
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Insert Length: 10000 Std Erro
Plate: 0117 row: N column: 19
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               Biomedical Polymers Research Bldg.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance. "
7 c 9 g 15 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0117N19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (http://www.jax.org/resources/documents/dnares/). The DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="E. Coli strain XL10-Gold, T1-resistant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Mouse 10kb plasmid UUGC1M library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAAATGAAATAAA
                                       Contact: Jeffery L. Miller
Laboratory of Chemical Biology
National Institute of Diabetes and Digestive and Kidney Diseases
Building 10, Room 9B17, National Institutes of Health, Bethesda,
20892_USA.
                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 49)
Gubin,A.N., Njoroge,J.M., Bouffard,G.G. and Miller,J.L.
Gene expression in proliferating human erythroid cells
Genomics 59 (2), 168-177 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AI630064 49 bp mRNA EST 08-MAR-2000 ad00157 Proliferating Erythroid Cells (LCB:ad library) Homo sapiens CDNA clone ad00157 random, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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Insert Length: 10000 Std Error: (
Plate: 0275 row: K column: 07
Seg primer: CACACAGGAAACAGCTATGACC
Tel: 301 402 2373
Fax: 301 435 5148
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Mouse 10kb plasmid UUGC2M library"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (http://www.jax.org/resources/documents/dnares/).
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/clone="UUGC2M0275K07"
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The 'ad' library was constructed by Alexander Gubin, Ph.D. in the Laboratory of Chemical Biology, NIDDK, NIH. DNA Sequencing and/or analyses by National Institutes of Health Intramural Sequencing Center (NISC). More information available at: http://hembase.niddk.nih.gov.
                                                                                                                                                                                                                                                                                                                                                   16 a
                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                     /dev_stage="Progenitor; EPO responsive CD71++++"
/lab_host="DH5alpha"
/lab_host="DH5alpha"
/note="Organ: blood; Vector: pCRII; Site_1: EcoRI; Site_2:
EcoRI; Human peripheral blood mononuclear cells were
cultured in the presence or absence of erythropoietin.
CD71++++ cells arising only in erythropoietin-supplemented
medium were isolated by fluorescence activated cell
sorting. Those cells demonstrated an average of six
additional doublings in suspension culture and erythroid
colony formation in methylcellulose. Suppression
subtractive hybridization was used to construct the ad
library (tester=sorted CD71++++ cells, driver=unsorted
cells cultured without erythropoietin)."

16 a 7 c 9 g 13 t 4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mononuclear Cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="blood"
/cell_type="Erythroid Cells"
/cell_line="Primary Culture of Peripheral Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ad00157"
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                                                                                                                                                                                                                              4.0%; Score 13;
100.0%; Pred. No.
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Maximum Match 100%
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1: /cgn2_6/ptodata/2

2: /cgn2_6/ptodata/2

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Best Local :
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APPLICANT: Johnso
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                                               1303 ТАЛАЛАТАЛАЛАЛАТАТАЛАЛАТАЛАЛАЛАТАТАЛАЛАТАЛАЛАЛАТАТАЛАЛАТАЛАЛАТ 1362
                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 6243 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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241 taaaaaaatttcagggggaatataaatgaaaaaattattcaaagtttactgtaatt 300
                                                                          181 aaaagtgtaaaataattattttattttaaatttgttaaaaatttgatataattgaattg 240
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                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 3770.4013
OTHER INFORMATION: /note= "RP4 origin of DNA transfer (oriT) from
OTHER INFORMATION: plasmid RP4"
                                                                                                                                                                                       61 gatatattaattatatagotgaaaatttataattatatgataagtatagttaataaataa 120
                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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                                                                                                                                                                                                                                      MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compate OPERATING SYSTEM: PC-DC SOFTWARE: PatentIn Relaction DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1483 TATAAAAGCCCATTTTTTTCAT 1505
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                             301 tttatgttttcatgttttcttat 323
182\, aaagtgtaaaataattatttttattttaaatttgttaaaaatttgatataattgaattgt\,\,241\,
                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Meigs, J. Timo REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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                                                                                                                                                                                                                                                                                                         ENGTH:
                                                                                 186, Application US/08998416
o. 6239264
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Knechtle, Philipp
Rebischung, Corinne
VENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
VENTION: AND USES THEREOF
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Steiner, Sabine
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SYSTEM: PC-DOS/MS-DOS
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24-DEC-1997
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52.1%;
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                                                                                                                                                    Score 61.8; DB Pred. No. 0.01;
                                                                                                                                        Mismatches 127;
                                                                                                                                                                 DB 4;
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                                                                                                                           Query Match
Best Local Similarity
                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                              TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                        15743
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ISraelsen New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-5EP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                            HYPOTHETICAL: I
                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: NI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                             MOLECULE TYPE:
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                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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                                                       92660
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Newport Beach
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                                                                                                                                                                                                                                                                     nucleic acid
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Sim, Kim L.
Chitnis, Chetan
Chitner, Louis H.
Miller, Louis H.
Creon, David S.
                                                                                                                                                                                                                                                                                   19124 base pairs
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Wellems, Thoma
                                                                                                               Conservative
                                                                                                                                                                                                                                          linear
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                                                                                                                           Score 61.6; DB 2
Pred. No. 0.0079;
                                                                                                               Mismatches
                                                                                                                                        DB 2;
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                                                                           US-07-867-106-2
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Matches 151;
              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                         TELEFAX: 215-568-3439 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15923 АААААТААААААТТТААТТАААТАААААААААТТАААТТАААТТААТТАСАТGCACATAT 15982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: PCT/AU90/00530
FILING DATE: 02-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Feeney, Joanne Longo
REGISTRATION NUMBER: 35,134
REFERENCE/DOCKET NUMBER: RICE-0002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
STREET: One Liberty Place 46th Floor
                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 5852 base pairs
                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 1992062 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Improved Plasmid Vectors for Cellular TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium
                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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                                                                                                                                                                                    ANTI-SENSE:
                                                                                                                                                                                                 MOLECULE TYPE:
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CITY: Philadelphia
                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US
FILING DATE: 19920625
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                                                                                                                                                                                                                              STRANDEDNESS:
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                                                                                                         NAME/KEY:
                                                                                                                                                                                                                 TOPOLOGY:
                                                                                           LOCATION:
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Williams, Keit
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            18.1%;
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Score 59.2; DB 1;
Pred. No. 0.021;
0; Mismatches 153;
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                                                                                                                                                    TELEFAX: (703) 816-41
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1638
                                             HYPOTHETICAL:
                                                            MOLECULE TYPE:
                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bancroft, Ian APPLICANT: Lister, Clare K TITLE OF INVENTION: Genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1578 ATTT 1575
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                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                      TYPE: ...
STRANDEDNESS: Quu.
STRANDEDNESS: Quu.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144
ORGANISM:
                                                                                                                                                                                                                                      NAME: Ms Mary J Wilson REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
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                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/GB96/01332
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Arlington
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                                                                                                                          9048 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Nixon & Vanderhye P.C.
1100 No. 6140085th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            United States of America
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Bancroft, Ian
   Brassica
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IBM PC compatible
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                                                              DNA (genomic)
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RESULT 7
US-08-998-416-1137/c
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Patent No. 6239264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                  TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 636 base pairs
TYPE: nucleic acid
                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           452 TCTTAATGAATTTATATAATTAAAAAAACGAATTTTAATTTAATCAGTGAAAAATTATATGTTA 393
                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 31-DEC
                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/0 FILING DATE: 24-DEC-1997
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                                                                                      TELEPHONE:
                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 T: 3054 Cornwallis RoadResearch Triangle Park: No. 6239264th Carolina
                                                                       919-541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pohlmann, Raines
Steiner, Sabine
Mohr, Christine
                                                                                                                                                                                                                                                                                                                                                             IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rebischung,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wendland, Jurgen
Knechtle, Philipp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Philippsen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                          919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No. 6239264artis Corporation
                                                                                                                                                                                                 UMBER: CH 0016/97
31-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ng, Corinne
GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
AND USES THEREOF
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53.5%;
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                                                                                                                                       38,241
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                                                                                                                         PF/5-30306/A/CGC1976
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TOPOLOGY: STRANDEDNESS:

linear

DNA (genomic) single

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Qγ
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Best Local Similarity 49.5
Matches 149; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 36, Application US/08883795A Patent No. 5985607
                                     APPLICATION NUMBER: US/08/883
FILING DATE: 27-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gravelle, Micheline
REGISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 7841
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1054-7311
TELECOMMUNICATION 1054-7311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
             TELEFAX: (416) 361-1398 INFORMATION FOR SEQ ID NO: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
ORIGINAL SOURCE:
ORGANISM: PAG
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Delcuve, General APPLICANT: Awang, Gregor
                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                 SOFTWARE:
                                                                                                                                                                                                                                               MEDIUM TYPE:
                                                                                                                                                                                                                                                                                   ZIP: M5H 3Y2
                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                STATE:
                                                                                                                                                                                                                                                                                                                                 CITY: Toronto
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                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATAAAAAGATTAAATAATATAAATCAACATAATATTTATAAAAATAGATATTATAATAA 393
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                                                                                                                                                                                                                                                                                                                                            40 King
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                                                                                                                                                                                                                                                                                                Canada
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49.5%;
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                                                                            7841-062
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                                                                                                                                                                                                     Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
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                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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CLONE: Rh 32
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ORIGINAL SOURCE:
                                                                          SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                CITY: Research Triangle Park
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                                                                                                                                                                      COUNTRY: U
ZIP: 27709
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VENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
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Knechtle, Philipp
                                                                                                                                                                                                                                                                                                                                                                              Pohlmann, Rainer
Steiner, Sabine
                                                                                                                                                                                                                                                                                                                                                                           Mohr, Christine
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                                             24-DEC-1997
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50.68;
                                                                                                                                                                                                                                                                                               AND USES THEREOF
                                                                                                                                                                                                                                                                               1152
CH 0016/97
                                                           US/08/998,416
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                                                                                          Version #1.30
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FILING DATE: 31-DEC-1996 ATTORNEY/AGENT INFORMATION:

PF/5-30306/A/CGC1976

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                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 33, Application Patent No. 6133506 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 52.1
Matches 149; Conservative
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TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/617,860B
                    FILING DATE: 01-MAR-PRIOR APPLICATION DATA:
                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: P.
                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Tvpfer, R., Bautor, J., Bothmann, H., Filsak, APPLICANT: Hvricke-Grandpierre, C., Klein, B., Martini, N APPLICANT: M ller, A., Schulte, W., Voetz, M., Walek, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 837 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Meigs, J. Timothy
REGISTON NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              266 AATAATATCTAATAATATTTTAATAACTAATTTAAAAATTTGAACATAGACTAAATAGTAT 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                   COMPUTER: IBM COM
OPERATING SYSTEM:
                                                                                                                                                                                                                   STREET: 1140 Ave
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86
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                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: sing
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                                                                                                                                                                                                                                                                             ADDRESSEE:
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                                                                                                                                                                                                                                                        1140 Avenue of the Americas
                                                                                                                                                                                                    USA
                                                                                                                             IBM Compatible
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                                                                                                                                                                                                                                                                             Steinberg,
                                                                                                                                              Diskette, 3.50 inch, 1.4 Mb storage
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                                     01-MAR-1996
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52.1%;
                                                                                                              DOS
                                                                                                                                                                                                                                                                                                                                Promoters
   PCT/EP94/02950
                                                                                                                                                                                                                                                                           Raskin & Davidson, P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 56.4; DB 4; Length 837; Pred. No. 0.07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
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                                                                                                                                                                                                                                                                                                                            RESULT 11
US-08-883-795A-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Дb
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                                                                                                                                                                                                                                                                                            Sequence 36, Application US/08883795A Patent No. 5985607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 53.2
Matches 143; Conservative
                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Delcuv
APPLICANT: Awang,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2750 Base pair
           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                          TITLE OF INVENTION: Recombinant DNA Molecules and Expression TITLE OF INVENTION: Vectors for Tissue Plasminogen Activator NUMBER OF SEQUENCES: 39
                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                               1745 AGGGCATAATAATCCATAAAACATTGTAA 1773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
ORGANISM: Cuphea lanceolata
                                                                                                    STATE: Opt-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1625 CAATTGAAATTATTACAAAATATATAATTAATAAAAATTAAATTTAAAGATAAATTTGT 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1565 ATTTTATTAAGTAAAAAAAAACTAAAAAAGTATTTGTAATTGGTTTTCAATTTTTCTCTT 1624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
LIBRARY: genom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL:
ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154 aaaggaaaatataaaatataaatttagataaaagtgtaaaaattaatt----atttttatttta 209
                                                                                                                                                                                                                                                                                                                                                                                                                           270 gaaaaaaattatttcaaagtttactgtaa 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
LOCATION:
                                                                               COUNTRY: Canada
ZIP: M5H 3Y2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIBRARY: genomic Lambda FIX II CLONE: ClTEg4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94 tatatgataagtatagttaataaataaatagtgttctcgggggacacttttttgttttaa 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 gtttaaatgaaataaagataataaaaagatatattaattaattaatatgctgaaaatttataat 93
                                                                                                                                              STREET:
                                                                                                                                                             ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 05-SEP-1994
APPLICATION NUMBER: DE P4329951.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AATTTTTTTAATACTTCGACTAATTTATTTTTCGTTTAATATATAAAAATTTTAGTTGAAA 1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 2750 Base pairs
                                                                                                               Ontario
                                                                                                                                           40 King Street West
                                                                                                                                                                                                                                               Awang, Gregor
                                                                                                                                                                                                                                                               Delcuve, Genevieve
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PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
2637..2750
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                                                                                                                                                               BERESKIN & PARR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 55.8; DB 3; Length 2750; Pred. No. 0.077; 0; Mismatches 122; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Moderat
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US-08-446-855A-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08446855A Patent No. 5849573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (416) 361-13 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                          APPLICANT: Stewart, APPLICANT: Flores, Maria V
APPLICANT: Flores, Maria V
APPLICANT: O'Sullivan, William J
APPLICANT: O'Sullivan, Wi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPULIVE TYPE: CUNA MOLECULE TYPE: CUNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 665 base pairs
                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 aaaagtgtaaaattaatttttattttaaattttgttaa----aaatttgatataattga 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 aaagtgttctcgggggacacttttttgttttaaaaaggaaaatataaaataaaatttagat 180
                       COUNTRY: USA
ZIP: 22201-4714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                              STREET: 1100 NO CITY: Arlington STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 40,261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/883,795A
                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aatttttatgttttcatgttttcttatt 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATGTTTATAAATAAATATTTTATAAATTAAAATGTTTATAATTACATATTTTATAATTAA 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             attgtaaaaaaaatttcagggggaatataaatgaaaaaaattatttcaaagtttactgt 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AATGTTTATAATTACATATTTATAATT 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gatatattaattatatagctgaaaatttataattatatgataagtatagttaataaataa 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
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                                                                                                                                                           E: Nixon & Vanderhye PC 1100 No. 5849573th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (416) 364-7311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 665;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    273
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                                                                                                                                                                                                                                                 US-09-150-741-1/c
Sequence 1, Application US/09150741
Patent No. 6183996
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               γy
                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
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                                                                                                                                                                  APPLICANT: Stewart et al.
TITLE OF INVENTION: Nucleotide Sequence Encoding Carbamoyl Phosphate
Patent No. 6183996
TITLE OF INVENTION: Synthetase II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 163; Conserv
                                                                CURRENT APPLICATION NUMBER: US/09/150,741
CURRENT FILING DATE: 1998-09-10
EARLIER APPLICATION NUMBER: PL5380
EARLIER FILING DATE: 1992-12-16
EARLIER APPLICATION NUMBER: AU93/00617
               EARLIER FILING DATE: 1993-12-02
EARLIER APPLICATION NUMBER: 08/446,855
EARLIER FILING DATE: 1995-07-06
                                                                                                                                                            FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
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NAME: Mitchard, Leonard C
                                                                                                                                                                                                                                                                                                                                                                                 8483 ACTTTT 8478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       322 attgtt 327
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 0 CLASSIFICATION:
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N: 435
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; SEQ ID NO 11
; LENGTH: 2251
; TYPE: DNA
; ORGANISM: Pinus taeda
US-08-991-677-11
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                                                                                                                                                                         Query Match
Best Local
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Best Local Similarity
Matches 163; Conserv
                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Production of Syringyl Lignin in Gymnosperms FILE REFERENCE: 506.7

CURRENT PELLCATION NUMBER: US/08/991,677A

CURRENT FILING DATE: 1997-12-16

EARLIER APPLICATION NUMBER: US 60/033,381

EARLIER FILING DATE: 1996-12-16

EARLIER FILING DATE: 1996-12-16

EARLIER FILING DATE: 1997-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Carraway, Daniel T
APPLICANT: Smeltzer, Richard H
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Chiang, Vincent L
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TYPE: DNA
ORGANISM: Plasmodium falciparum
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                                                                                          322 attgtt 327
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53.3%;
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US-07-867-106-2
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                                                          Best Local Similarity Matches 124; Conserv
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                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:

APPLICATION NUMBER: AU PJ 7187

APPLICATION NUMBER: PCT/AU90/00530

FILING DATE: 02-NOV-1989

ATTORNEY/AGENT INFORMATION:

NAME: Feeney, Joanne Longo
REGISTRATION NUMBER: 35,134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 5852 base pairs
TYPE: NUCLEIC ACID
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                                                                                                                                                                                        LOCATION: FEATURE:
                                                                                                                                                                                                                      FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
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ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
STREET: One Liberty Place 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                      ANTI-SENSE:
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776 aacactattattttaa
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              40 atgaaataaagataaataaaaagatataattaattaatagctgaaaatttataattatatag 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: U: FILING DATE: 19920625
                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                                                                         LOCATION:
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                                                            Conservative
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51.7%;
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Improved Plasmid Vectors for Cellular
Olimo Moulds of the Genus Dictyostelium
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                                                                         Score 54.4; DB 1;
Pred. No. 0.12;
                                                            Mismatches 116;
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                                                                                        Length 5852;
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Search completed: January 24, 2002, 02:18:46 Job time: 3919 sec

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Title:
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BC
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length: 50
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327
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/SIDS2/gcgdata/geneseq/geneseqn/NA1983.DAT:*
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Copyright (c) 1993 - 2000 Comp
/SIDS2/gcgdata/geneseq/geneseqn/NA1989.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn/NA19890.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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16 16 16 16 15 15 15	Score
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AAT42655 AAA51200 AAZ27689 AAT97603 AAZ90775 AAZ68379 AAZ68379 AAA66183 AAH46804 AAT394457 AAQ43975	ID
Primer for amplify N-terminal primer PCR primer for Ver Shiqella dysenter! Primer Y104F. Syn Human map-related Dog genomic marker Human high motilit Hel-N2 selected se Human Hel-N2 select	Description

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45	44	43	42	41	40	39	38	37	36	35 5	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12
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4.0	4.0	4.0	4.0	4.0	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.3	٠. س	4.3	4.3	4.3	4.ω	4.3	4.3	4.3	4.3	4.3	4.3	4.3	Carred Carred	4.6
17	_		,	15	5	47	47	47	47	47	45	4 5	45	45				32		31	29	29	27	26	26	22	22	٠	181			18	48
16	21	22	22	22	21	21	21	21	21	21	22	22	22	22	15	22	18	20	19	16	21	17	19	19	19	22	22	20	μ' W	ω	13	ű	16
AAQ92084	AAA57758	AAF48099	AAF48098	AAF48097	AAA98312	AAZ67813	AA267549	AAZ67533	AAZ67473	AAZ66366	AAC88875	AAC88874	AAF55450	AAF55449	AAQ62952	AAC90606	AAT97603	AAZ27689	AAV67854	AAT25703	AAA51200	AAT42655	AAV07937	AAV07922	AAV07952	AAS01643	AAS01590	AAZ22162	AAQ30310	AAQ30311	AAQ20160	AAQ20161	AAT25576
Renilla reniformis	Nucleotide sequenc	IGFBP3 oligonucleo	IGFBP3 oligonucleo	IGFBP3 oligonucleo	Human MSH6 fragmen	Human map-related	Oligonucleotide TA	Oligonucleotide TA	Oligonucleotide us	Oligonucleotide us	 Glycophorin antibo 	Tomato spotted wil .	Ч'	PCR primer for Ver		Human gene signatu		Primer for amplify	1		Helicobacter pylor	Human IQGAP2 54-ta	Human IQGAP2 CpG i	Human c-IAP-1 mRNA		Oligomer HSV724 fo	Cross-linking olig	-linking	Human gene signatu				

RESULT AAT42655 Primer for amplifying verotoxin (VT-1) subunit A coding sequence. AAT42655; AAT42655 standard; DNA; 29 (OPHI-) OPHIDIAN PHARM INC. WO9630043-A1 Synthetic Verotoxin; Escherichia coli; enteric infection; diarrhoea; vaccine; 24-MAR-1995; 25-MAR-1996; 25-FEB-1997 (first entry) 03-OCT-1996 haemolytic uraemic syndrome; 95US-0410058 96WO-US04093. ВP detection; ss

ALIGNMENTS

Compsn. contg. neutralising antitoxin against E.coli vero-toxin used to treat intoxicated individuals, and as a prophylactic against diarrhoeal disease or extra-intestinal complications of E.coli infection

WPI; 1996-505779/50.

Carroll SB,

Padhye NV, Stafford

Example 6; Page 58; 101pp; English

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RESULT
AAA51200
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Best Local Similarity
to convert the signal sequence methionine codon into a NdeI site to allow cloning of the amplified genes into the vector without addition of vector-encoded amino acids. The C-terminal primers comprises the C-terminal 7 codons of each gene fused to the sequence CTCGAGCC, in order
                                                               E. coli verotoxin (VT) type 1 and 2 subunits A and B were cloned into pET-23b, designed to allow expression of the native proteins containing C-terminal polyhistidine tags. The VT-1 and VT-2 genes were engineered
                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preferably a fusion protein containing a non-VT protein sequence are part of the E.coli VTl or VT2 sequence. Two primers (AAT42655, AAT42656) were used to amplify the verotoxin VT-1 A subunit coding sequence and add a histidine tag coding sequence to the subunit sequence. Two primers (AAT42655, AAT42658) were used to amplify the verotoxin VT-1 A and B subunits and add a histidine tag coding verotoxin VT-1 A and B subunits and add a histidine tag coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Compositions containing neutralising antitoxin against one or more E. coli verotoxin (VT) can be used to treat intoxicated adults and children with enteric bacterial infections. They may also be used as prophylactics e.g. as a vaccine, against diarrhoeal disease or the development of extra-intestinal complications of E.coli infection,
                                                                                                                                  Example
                                                                                                                                                                                  quantities useful for
                                                                                                                                                                                                                                                               Williams JA,
                                                                                                                                                                                                                                                                                                                             24-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                           13-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                          27-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                       US6080400-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prımer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VT-1; verotoxin; antitoxin therapy; fusion protein; affinity tag;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-terminal primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA51200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA51200 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       especially haemolytic uraemic syndrome. The antitoxin can also be used to detect E. coli VT in a sample. The VT is recombinant,
                                                                                                                                                                                                                                                                                              (OPHI-) OPHIDIAN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 aaaataattatttta 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
                                                                                                                                  6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polyhistidine;
                                                                                                                                                              cell for recombinantly expressing bacterial toxins in large s useful for immunization and treatment of bacterial s, comprises expression vector encoding bacterial toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29 BP; 11 A; 2 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to the subunit sequences.
                                                                                                                                 Column
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   production; screening; dairy; anti-bacterial; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first
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                                                                                                                                                                                                                                                                                                                          95US-0410058
                                                                                                                                                                                                                                                                                                                                                         97US-0816977
                                                                                                                                  83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for E. coli verotoxin 1 subunit A gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
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                                                                                                                               83pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ss.
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                                                                                                                                  English.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amplify the
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      in order
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Sequence

32 BP; 12 A;

2 C;

4

G;

14 T;

0 other;

using the

oligonucleotide of the invention. transfer of a foreign DNA fragment. amplification of VT gene from environments.

oligonucleotide is useful

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Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to add the polyhistidine tag. The primers delete the native stop codons, and when cloned into pET-23 add a C-terminal extension of Leu-Glu-(His)6. WT B chains are small proteins (approximately 8 kDa), so use of a small affinity tag was preferred (i.e. polyhistidine). A polyhistidine affinity tag facilitates single step affinity purification of subunits from periplasmic extracts. However, due to poor recovery of his-tagged WT-1 A and WT-2 A chains, expression of maltose binding protein (MBP) fused subunits was undertaken. Due to the toxicity of the WT-2 B subunit, strict uninduced promoter control is necessary to permit cell viability. Bacterial host cells expressing a recombinant expression vector encoding a polyhistidine affinity tag and a portion of the WT-2 B chain are claimed. The vector is chosen from pET24V12B, where "L+" indicates that the vector encodes the mature form of the protein and "L-" indicates that the vector encodes the mature
                                                                                        This used
                                                                                                                                                                                                                                                                                                                                           14-SEP-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       form of the protein. The bacterial cell is capable of expressing large quantities (40 mg/l) of VT-2B. The toxins are useful for immunizing non-mammals and for detecting bacterial toxins in environmental samples
                                                                                                                                   Claim 11; Page 9; 10pp; Japanese
                                                                                                                                                                  fragment
                                                                                                                                                                                                An oligonucleotide for
                                                                                                                                                                                                                                WPI; 1999-603716/52
                                                                                                                                                                                                                                                                                          27-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                   JP11243996-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Verotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ27689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                  detection
                                                                                                                                                                                                                                                              (тоум ) тоуово кк.
                                                                                                                                                                                                                                                                                                                       27-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCR primer for Verotoxin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ27689 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          including soil, water, industrial sample obtained from food and dairy processing
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                                       sequence represents a PCR primer of the invention. The primer for amplification of the E. coli verotoxin (VT) gene. The onucleotide is useful for detection of inactivated VT gene by sfer of a foreign DNA fragment. Simple, rapid and specific ification of VT gene from environmental factors is achieved us
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aaaataattatttta
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                                                                                                                                                                                  inactivated
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                                                                                                                                                                                                                                                                                            98JP-0047677.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24
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                                                                                                                                                                               amplification of verotoxin -
ed verotoxin gene by transfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          industrial samples,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32 BP
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                                                                                                                                                                                                                        dysenteriae 1 delta-stxA allele. The delta-stxA allele was integrated into delta-guaB-A of delta-guaB-A, delta-virG S. dysenteriae 1, which inactivated the shiga toxin of this strain. The mutant can be used in the preparation of vaccines such as, a live vector vaccine comprising a Shigella mutant, (which encodes and expresses a foreign antigen, and a pharmaceutically acceptable carrier) or DNA mediated vaccine comprising the Shigella mutant (which also contains a plasmid which encodes and expresses a foreign antigen in a eukaryotic cell). The
                                                                                                                                                                                                                                                                                                                  This is a PCR primer used in the amplification of the Shigella dysenteriae 1 delta-stxA allele. The delta-stxA allele was in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT97603;
             AAV90775 standard; DNA; 39
                                                                                                                                                                                        Sequence 36
                                                                                                                                                                                                                vaccines can be used against Shigellosis.
                                                                                                                                                                                                                                                                                                                                                       Example 6; Page 57; 94pp;
                                                                                                                                                                                                                                                                                                                                                                                Shigella mutants with mutation in guaB-A – used in vaccines against \operatorname{Shigellosis}
                                                                                                                                                                                                                                                                                                                                                                                                                                               Levine MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYMA-) UNIV MARYLAND BALTIMORE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9737685-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
Shigella dysenteriae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Delta-virG allele; delta-guaB-A allele; PCR; amplification; primer; delta-stxA allele; shigellosis; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shigella dysenteriae delta-stxA allele PCR primer 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT97603 standard; DNA;
                                                                                     189 aaaataattatttta
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                                                                           14
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                                                                                                                          l Similarity
16; Conserv
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Similarity 100.0%;
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                                                                                                                                                                                       11 A; 3 C;
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                                                                                                                                    100.0%;
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                                                                         29
                                                                                                                                                  4.9%;
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                                                                                                                                                                                                                                                                                                                                                        English.
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                                                                                                                                     Score 16;
Pred. No.
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Pred. No.
                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                    DB 18;
1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 20;
1e+03;
                                                                                                                          0
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                                                                                                                                               Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                          Indels
                                                                                                                         0;
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                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                         0
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20
                                                                                                                                                                                                                                                                                                                                                                       AAZ68379
                                                                                                                                                                                                                                                           Вb
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 16; Conserv
                                                           Human genome; biallelic marker; high density disequilibrium map; genomic map; haplotype; phenotype; polymorphic base; genotyping; haplotyping; hybridisation; identification; characterisation; diagnosis; single nucleotide polymorphism; SNP; ds.
                                                                                                                                                                                                                                                                                                                                                                                            previously unrecognised immunogenic cluster families. H. pylori antigens are used to detect H. pylori-specific antibodies, for diagnosing infection or to confirm eradication of infection, and in vaccines to protect against H. pylori infection and related diseases (gastritis, peptic ulcer, gastric adenocarcinoma/lymphoma). The present primer is used in the course of the invention.
                                                                                                                                               10-SEP-2001
                                                                                                                                                                                              AAZ68379 standard; DNA; 47 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim Disclosure; Page 194; 402pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Helicobacter pylori antigens and related nucleic acid sequences - useful in serological diagnosis and protective vaccines, providing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chow TP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antigen; immunogenic cluster family; vaccine; peptic ulcer; gastric adenocarcinoma; gastric
 variation
                                                                                                                       Human map-related biallelic marker SEQ ID NO:2726
                                                                                                                                                                                                                                                                                                                                                                       Sequence 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proteins that are characterised by immunoreactivity with H. pylori-positive antisera. The specification also describes 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-009433/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9849314-A2
                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              long-lasting immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENE-) GENELABS TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-OCT-1997;
25-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primer Y104F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-FEB-1999
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                                                                                                                                                                                                                                                                                                                                                                      BP; 15
                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KΕ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-0061958.
97US-0045107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98WO-US08487.
Location/Qualifiers replace(24,A)
                                                                                                                                                                                                                                                                                                                                                                      A; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               which describes Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lim MY,
                                                                                                                                                                                                                                                                                                                       4.9%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                      Ç
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McAtee CP;
                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                                                                                                                      G;
                                                                                                                                                                                                                                                                                                                        Score 16;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                      Η,
                                                                                                                                                                                                                                                                                                                                                                         0 other;
                                                                                                                                                                                                                                                                                                                       DB 20;
1e+03;
                                                                                                                                                                                                                                                                                                                                  20;
                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gastritis; diagnosis;
lymphoma; primer; ss.
                                                                                                                                                                                                                                                                                                                                 Length 39;
                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          providing
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                                                                                                                                                                                                                                                                                                           Gaps
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RESULT
AAA66183
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ65654 to AAZ69578 represent human biallelic markers from the present invention, which contain a polymorphic base at position 24 of their nucleotide sequences. AAZ69579 to AAZ77440 represent amplification primers for the biallelic markers. The biallelic markers of the invention have a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and diagnostic methods, as well as the characterisation of the differential efficacious responses to and side
                                                                                                       Dog; genome; genomic chromosome location; phenotype; behaviour;
15-NOV-1999;
                          25-MAY-2000
                                                     WO200029615-A2
                                                                               Canis familiaris
                                                                                                                                                          Dog genomic
                                                                                                                                                                                      09-OCT-2000
                                                                                                                                                                                                                 AAA66183;
                                                                                                                                                                                                                                           AAA66183 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 47 BP; 24 A; 5 C; 6 G; 12 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                effects from pharmaceutical agents acting on a disease as well as other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel biallelic markers used to construct a high density disequilibrium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-013267/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cohen D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-APR-1998;
23-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09954500-A2
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                                                                                                                                                                                                                                                                                                                                       147
                                                                                                                                                                                                                                                                                                             13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3367, are not actually given a sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of the human genome
                                                                                                                                                                                                                                                                                                                         gttttaaaaaggaaaa 162
                                                                                                                                                                                                                                                                                                          gttttaaaaaggaaaa 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The SEQ ID NOS 2852, 2913, 2974, 3035,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 812; 2745pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Blumenfeld
                                                                                                        y, genomic marker; radiation hybrid map; identification;
location; gene marker; polymorphic microsatellite marker;
behaviour; pedigree; ss.
                                                                                                                                                            marker oligonucleotide sequence SEQ
                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                      (first entry)
 99WO-IB01907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0082614.
98US-0109732.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /standard_name= "single nucleotide polymorphism"
                                                                                                                                                                                                                                                                                                                                                                             4.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chumakov
                                                                                                                                                                                                                                           ВP
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                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                              Score 16;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                              DB 21; 1
9.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in the
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                                                                                                                                                             IJ
                                                                                                                                                                                                                                                                                                                                                                                          Length 47;
                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                             NO:45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence Listing
                                                                                                                                                                                                                                                                                                                                                                0;
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RESULT
AAH46804
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for identifying and localising dog genes, since it covers approximately 80 % of the dog genome and provides a dense map integrating different types (i.e. Type I and Type II) of markers. The map and the dog genome markers (or complementary sequences) are especially useful to identify genes responsible for phenotypic and behavioural traits in dogs, to identify morbid genes, to analyse diseases and identify implicated genes in such diseases and their alleles, and to study dog pedigrees. They may also be useful for isolating corresponding human gene sequences e.g. genes involved in genetic diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Canine familiaris) genome comprising the genome location of a marker selected from AAA66139 to AAA66942. The radiation hybrid map is useful
                                        WPI; 2001-418226/44
                                                                                                                                                                                                                                                                                                Human; high motility group protein family 11; cancer; haemopathy;
HIV infection; immune disease; inflammation; gene therapy;
                                                                                                                                                                                                                                                                                                                                           Human high motility group protein family 11 cDNA PCR primer #2.
                                                                                                                                                                                                                                                                                                                                                                         19-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 14 A; 1 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 55; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New radiation hybrid map of the dog, Canine familiaris, genome, useful for e.g. identifying genes implicated in phenotypic and behavioral traits or in genetic diseases and for studying dog pedigrees
                                                                                               (UYFU-) UNIV FUDAN.
(SHAN-) SHANGHAI BIO
                                                                                                                                           23-DEC-1999;
                                                                                                                                                                     18-DEC-2000; 2000WO-CN00595
                                                                                                                                                                                                 05-JUL-2001.
                                                                                                                                                                                                                             WO200147967-A1
                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                   PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                AAH46804 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a radiation hybrid map of the dog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  261 aatataaatgaaaaa 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l aatataaatgaaaaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Andre C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CENT NAT
                                                                                                                                           99CN-0125721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0108193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.6%;
100.0%;
                                                                                                DOOR GENE TECHNOLOGY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 15;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
2.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .7e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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0

High motility group protein applicable in diagnosis and

family 11 treatment

and encoded polynucleotide,
of cancer, haemopathy, HIV

Example infection,

Page 17;

39pp;

Chinese

immunological diseases and various inflammation

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RESULT
AAT39439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
        The sequences given in AAT39427-46 represent random oligonucleotides which were isolated due to their ability to bind to the human neuron-specific protein, Hel-N2. These sequences contain short stretches of uridylate residues interspersed with other residues. These Urich regions share homology with the 3'-UTR instability sequences.
                                                                                                          Prodn of cDNA library mRNA with RNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                             paraneoplastic sensory neuropathy; oncoprotein; lymphokine; rat; elav; RNA recognition motif; RRW, Drosophila; cellular growth; localisation; instability; translatability; neurons; autoimmune protein; PE; PCD; PSN central nervous system; cancer; paraneoplastic cerebellar degeneration; paraneoplastic encephalomyelitis; RNP-1 octamer sequence; human elav-like neuronal protein-1; ss.
                                                                                                                                                                                                                     15-SEP-1993;
11-MAY-1992;
                                                                                                                                                                                                                                                                                                        US5525495-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides the protein and coding sequences of the human high motility group protein family 11. The sequences are useful the treatment of cancer, haemopathy, HIV infection, immune diseases and inflammation. The present sequence is a PCR primer for the coding
                                                                                                                                                                                              ( - nd 3n)
                                                                                                                                                                                                                                                         11-may-1992;
                                                                                                                                                                                                                                                                                 11-JUN-1996
                                                                                                                                                                                                                                                                                                                                                        misc_RNA
                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hel-N2 selected sequence, e-13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT39439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT39439 standard; RNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 taattattttattt 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            taattatttttattt 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neuron-specific protein; Hel-N1; 3'-UTR instability sequence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 Similarity 100 15; Conservative
                                                                                                                                                                                              UNIV DUKE
  found in mRNA's.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the invention
                                                                                    Fig 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                      JD,
                                                                                                                                                                                                                     93US-0120827.
92US-0881075.
                                                                                                                                                                                                                                                         92US-0881075
                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers 15..23
                                                                                                                                                                                                                                                                                                                            /*tag= a
/note= "Consensus sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Α;
                                                                                                                                                                      Levine
                                                                                  66pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                          for related proteins - by protein Hel-N1 or Hel-N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.68;
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                                                                                   English.
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Instability sequences are target elements
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                      screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                      total
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSN;
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Disclosure;

Fig

11;

67pp;

English

proteins containing

from total cell mRNA.

members

encoding

structurally

or functionally related

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RESULT 1
AAV37457
ID AAV3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                             15-SEP-1993;
11-MAY-1992;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     which may indicate a correlation with rapid growth. Hel-Nl cDNA was isolated by probing for rat and human elav counterparts using degenerate primers designed to simulate the RNP-l octamer sequence present in two of the three RNA recognition motifs (RRM's) of Drosophila elav. Hel-Nl was found to contain 3 RRM's, where the third one (see also AAW00244) is sufficient for mRNA 3'-UTR binding activity. Full length Hel-Nl, when transfected into a cell, causes cellular growth to cease, however, if just the third binding domain is transfected into cells, the cells undergo rapid growth. Hel-Nl binds as a multimer along the mRNA, presumably enhancing its localisation, instability and/or regulating it translatability and/or deadenylating it. This protein may be responsible for the growth cessation of neurons. Hel-Nl is an autoimmune
                                                                                                                          Gao F,
                                                                                                                                                     (GAOF/)
(KEEN/)
(LEVI/)
                                                                                                                                                                                                                                                                                                                                                                                                    Growth regulatory protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                which reside in the 3'-non-coding regions of mRNA's which encode oncoproteins and lymphokines. Hel-N2 is a deleted form of Hel-N1 in which the residues 239-251 have been deleted. This protein is expressed in medulloblastoma tumour cells and is not found in whole human brain. A small amount of Hel-N2 is also found in fetal brain,
                                                                   Use of proteins which bind RNA - for obtaining a cDNA library
                                                                                               WPI; 1998-387003/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV37457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein in certain patients who show central nervous system manifestations of cancer called paraneoplastic cerebellar degeneration (PCD), paraneoplastic encephalomyelitis (PE) or paraneoplastic sensory
                                                                                                                                                                                                                                                                       07-JUN-1995;
                                                                                                                                                                                                                                                                                                  30-JUN-1998
                                                                                                                                                                                                                                                                                                                               US5773246-A
                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                      chromosome mapping; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                Human Hel-N2 selected RNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neuropathy (PSN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197 tatttttattttaaa 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 uauuuuuauuuuaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10
                                                                                                                                                                    GAO F.
KEENE J
                                                                                                                          Keene JD,
                                                                                                                                                       LEVINE T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                             93US-0120827.
92US-0881075.
95US-0478675.
                                                                                                                                                                                                                                                                      95US-0478675
                                                                                                                                                                      D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Α,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNA;
                                                                                                                            Levine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 G;
                                                                                                                                                                                                                                                                                                                                                                                   Hel-N2; oncogene; cytokine; lymphokine; functionally related protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No. 2.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                  e-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 27;
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RESULT 11
AAQ43975 .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
           The sequence is that of an oligonucleotide, III, which is able to form a triple helix with a duplex nucleic acid (dsNA) contg. a target sequence which comprises at least one pyrimidine tract, and at least one adjacent purine tract. It is useful for therapeutic or diagnostic control of gene expression, e.g. suppression of mRNA
diagnostic control of gene expression, e.g. suppression \boldsymbol{\xi}
                                                                                                                                                                                       Disclosure;
                                                                                                                                                                                                                                                             New oligo:nucleotide(s) forming triple helix with target nucleic acid - contain purine and pyrimidine tracts in specific orientations, useful therapeutically or diagnostically e.g. (for
                                                                                                                                                                                                                                                                                                                                                                                                                                        Jayasena SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-DEC-1991;
21-JAN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9312230-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnostic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Triple helix forming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ43975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ43975 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 27
                                                                                                                                                                                                                                           inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (STRI ) SRI INT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Purine; pyrimidine; tracts; intramolecular triplex; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               197 tatttttattttaaa 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity hes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 uauuuuuauuuuaaa
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                                                                                                                                                                              Page 48; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             control;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP; 7 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                           HIV RNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Johnston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91US-0808452.
92US-0826934.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92WO-US10792.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oligonucleotide III.
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33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene expresssion; mRNA synthesis suppression;
                                                                                                                                                                                                                                              etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                           BH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 G; 16 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 15;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .6e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Sequence

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Best Local s
Matches 15
                         3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.
                                                                                                                                                                        A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in AAT19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene signature; messenger RNA; mRNA; relative abundance; frequency human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               synthesis from a target gene. A specified application is targetting of RNA in the HIV-1 genome. When appropriately labelled it may also be used as a probe. Attachment of cleavage agents caused permanent inactivation of the target by site-specific cleavage.
                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                       Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT25576 standard; cDNA to mRNA; 48 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 30 BP; 12 A; 0 C; 5 G; 13 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Matsubara K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09514772-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (OKUB/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MATS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212 tttgttaaaaatttg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 tttgttaaaaatttg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  typing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
                                                                                                                                                                                                                                                                                           ۲
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MATSUBARA K.
                                                                                                                                                                                                                                                                                         Page 1862; 2245pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     signature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                          Okubo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93JP-0355504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94WO-JP01916.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUMGS07754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 15; DB Pred. No. 2.6 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 14; 1
2.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    frequency;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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RESULT :

13

AAQ20161 standard; DNA; 18

ВP

Вþ οy

17 aaaatataaataaaa 31

aaaatataaataaaa 173

159

Query Match
Best Local Similarity
Matches 15; Conserva

4.6%; S llarity 100.0%; Conservative 0;

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deoxyribonucleic acid; major groove; HSV;
inverted polarity region; covalent cross-linking group; ss
                 /*tag= k
/mod_base= OTHER
/note= "N-methy1-8-oxo-2'-deoxyadenine"
                                                                                                                                                                                                                                                                                                                                                                             /*tag= d
/mod_base= OTHER
/note= "N-methyl-8-oxo-2'-deoxyadenine"
                                                                                                                               /mod_base= OTHER
/mote= "N-methyl-8-oxo-2'-deoxyadenine"
                                                                                                                                                                                     /mod_base= OTHER
/note= "N-methyl-8-oxo-2'-deoxyadenine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                  'note= "N-methyl-8-oxo-2'-deoxyadenine'
                                                                                                                                                                                                                                          "N-methyl-8-oxo-2'-deoxyadenine"
                                                                                                                                                                                                                                                                                              "N-methyl-8-oxo-2'-deoxyadenine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    "N-methyl-8-oxo-2'-deoxyadenine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "N-methyl-8-oxo-2'-deoxyadenine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "N4N4-ethanocytosine"
                                                                                          inverted_polarity_region
see comments"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 15;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               target Herpes Simplex Virus
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2.5e+03;
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 AAQ20160
AAQ2
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KW deox
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                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This oligomer contains an inverted polarity region formed from an o-xyloso dimer synthon. Residues II and I2 are linked via an o-xyloso group (i.e. nucleotides that have xylose sugar linked via the o-xylene ring). The sequence is designed to target the Herpes Simplex virus I beginning at nucleotide 10996 and to covalently
                       modified_base
                                                                                                                  Synthetic
                                                                                                                                                                               Cross-linking oligomer 723 to target Herpes
                                                                                                                                                                                                        01-APR-1992
                                                                                                                                                                                                                                 AAQ20160;
                                                                                                                                                      deoxyribonucleic acid; major groove; HSV;
                                                                                                                                                                                                                                                         AAQ20160 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18 BP; 12 A; 1 C; 0 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                cross-link to it. See also AAQ20151-Q20160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New sequence-specific non-photo-activated crosslinking agents bind to the major groove of duplex DNA and are esp. useful for treating latent infections e.g. \rm HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1992-007480/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-JAN-1991;
25-MAY-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified_base
                                                                           modified_base
                                                                                                                                        inverted polarity region; covalent cross-linking group; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matteucci MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-MAY-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GILE-) GILEAD
                                                                                                                                                                                                                                                                                                                                                                          14;
                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Krawczyk S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91US-0640654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCIE INC
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17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "N-methyl-8-oxo-2'-deoxyadenine"
15
/mod_base= OTHER
                                     /mod_base= OTHER
/note= "N-methyl-8-oxo-2'-deoxyadenine"
                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note=
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                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
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                                                                                                                                                                                                                                                          ВP
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                                                                                                                                                                                                                                                                                                                                                                                   Score 14; DB 13;
Pred. No. 6.9e+03;
                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                             Simplex Virus
                                                                                                                                                                                                                                                                                                                                                                                               Length 18;
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Key Synthetic Cross-linking

724 to

01-APR-1992 AAQ20161

(first entry) oligomer

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/mod_base= OTHER

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0;

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New sequence-specific non-photo-activated crosslinking bind to the major groove of duplex DNA and are esp. use treating latent infections e.g. \rm HIV
This oligomer contains an inverted polarity region formed o-xyloso dimer synthon. Residues 11 and 12 are linked via \epsilon
                        Example 4; Page 29; 42pp; English.
                                                                  WPI; 1992-007480/01
                                                                                 Matteucci
                                                                                                            14-JAN-1991;
25-MAY-1990;
                                                                                                                                24-MAY-1991;
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                                                                                               GILEAD
                                                                                MD,
                                                                               Krawczyk S;
                                                                                               SCIE INC.
                                                                                                             91US-0640654
90US-0529346
                                                                                                                                91WO-1003680
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/mod_base= OTHER
/note= "N-methyl-8-oxo-2'-deoxyadenine"
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/mod_base= OTHER
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/note= "N-methyl-8-oxo-2'-deoxyadenine"
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/mod_base= OTHER
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/note= "N-methyl-8-oxo-2'-deoxyadenine"
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inverted_polarity_region
"see comments"
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                                            are esp. useful for
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RESULT 15
AAQ30311
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Best Local S
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the o-xylene ring). The sequence is designed to trarget the Herpes
Simplex virus I beginning at nucleotide 10996 and to covalently
cross-link to it. See also AAQ20151-Q20161.
                                     modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligomer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-DEC-1992
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                                                                                    modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity hes 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 aaaatataaataaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                            /*tag= i
/mod_base=
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/mod_base= OTH
/note= "OTHER=
/*tag= j
/mod_base= OTHER
/note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
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/mod_base=
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/note= "OTHER=
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ER= N4
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Pred. No.
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Mismatches 0;
                                                  methyl-8-oxo
                                                                                                                                                                                                 methyl-8-oxo
                                                                                                                                                                                                                                                                                                                                                                                          methyl-8-oxo 2' deoxyadenine"
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                                                  deoxyadenine"
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Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                              The synthetic oligomer is capable of forming a triplex at physiological pH with a purine rich target sequence by coupling into the major groove of the duplex. The specific target sequence of this oligomer is a herpes simplex virus I duplex beginning at nucleotide 10996 contg. a purine-rich region concentrated on one chain of the duplex. The oligomer, and others like it are useful in diagnossis and therapy of diseases characterised by specific DNA duplex targets, e.g. respiratory syncytial virus, HIV, hepatitis, herpes, malignant tumours and inflammation. The triple helices form
                                                                                                                                                                                                                                                                                                                                                                                                            17-APR-1991;
17-APR-1991;
27-SEP-1991;
                                                                                                 contains an inverted polarity region formed from an o-xyloso dimer synthon. The linking gp. is o-xyloso (nucleotides have the impositions of xylose sugars linked via the o-xylene ring). Two nucleotides are coupled through a xylene residue to form the dimer synthon. This additional modifications may render the oligomer state outlease activity. The oligomer is able to inhibit gene express
                                                                               to nuclease activity. The oligons verified by in vitro systems see also AAQ25452-25501 and AAQ
                                                                                                                                                            under mild conditions thus assays may be carried out without subjecting the test specimen to harsh conditions. The oligomer
                                                              Sequence
                                                                                                                                                                                                                                                                                    Claim 12; Page 67; 77pp; English
                                                                                                                                                                                                                                                                                                                 New oligomers contg. modified bases - which form a triplex with G-C doublet in a DNA duplex, for treating and diagnosing HIV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-NOV-1990;
18-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                         hepatitis,
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                                                                                                                                                                                                                                                                                                                                                                    Froehler B,
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                                                              18
                                                                                                                                                                                                                                                                                                        herpes, malignancy and inflammation
                                                              BP;
             Conservative
                                                                                                                                                                                                                                                                                                                                                                    Krawczyk S,
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91US-0686546.
91US-0686547.
91US-0766733.
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91US-0643382.
91US-0683420.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91WO-US08811
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                                                              12 A; 1 C; 0 G; 5 T; 0 other;
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'label= inverted_polarity_region
'note= "see comments"
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         4.3°; P1
100.0%; P1
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HER= N6
                     Score 14;
Pred. No.
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ER= N6
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                                                                                  AAQ30226-448.
            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          methyl-8-oxo
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                                DB 13;
                      6.9e+03;
                                                                                                                                                                                                                                                                                                                                                                    Milligan
                                                                                                  render the oligomer stable
to inhibit gene expression
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                              Length 18;
            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oligomer HSV723 for forming triplex with HSV target duplex
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RESULT 17
AAZ22162/c
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contains an inverted polarity region formed from an o-xyloso dimer synthon. The linking gp. is o-xyloso (nucleotides have the 3' positions of xylose sugars linked via the o-xylene ring). Two nucleotides are coupled through a xylene residue to form the dimer synthon. This additional modifications may render the oligomer stable to nuclease activity. The oligomer is able to inhibit gene expression, as verified by in vitro systems.

See also AAQ25452-25501 and AAQ30226-448.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-APR-1991;
17-APR-1991;
27-SEP-1991;
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18-JAN-1991;
08-APR-1991;
26-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        physiological pH with a purine rich target sequence by coupling into the major groove of the duplex. The specific target sequence of this oligomer is a herpes simplex virus I duplex beginning at nucleotide 10996 contg. a purine-rich region concentrated on one chain of the duplex. The oligomer, and others like it are useful in diagnosis and therapy of diseases characterised by specific DNA duplex targets, e.g. respiratory syncytial virus, HIV, hepatitis, herpes, malignant tumours and inflammation. The triple helices form under mild conditions thus assays may be carried out without subjecting the test specimen to harsh conditions. The oligomer
                                                                    AAZ22162;
                                                                                                                        AAZ22162 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; Page 67; 77pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hepatitis, herpes, malignancy and inflammation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oligomers contg. modified bases - which form a triplex with doublet in a DNA duplex, for treating and diagnosing HIV,
                                                                                                                                                                                                                                                                                 aaaatataaataaa
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                                                                                                                                                                                                                                                                                                                                                              Conservative
             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oligomer is capable of forming a triplex at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91US-0686546.
91US-0686547.
91US-0766733.
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910S-0686544.
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91US-0643382.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; 0 C;
                                                                                                                                                                                                                                                                                                          172
                                                                                                                                                                                                                                                                                                                                                                                    4.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "see
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inverted_polarity_region
"see comments"
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                                                                                                                        BP.
                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                       Score 14;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                       DB 13; I
6.9e+03;
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                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                            Length 18;
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RESULT 1
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Best Local S
Matches 14
                                                                    apolipoprotein B; APOB; caudal type homeobox transcription factor 2; CDX2; epidermal growth factor receptor; EEFR; fibrillin-1; FBN1; G protein-coupled receptor 37; GPR37; heat shock 70kD protein 6; HSP70B'; HSPA6; RasGAP-related protein; IQGAP2; proteinase-activated receptor 2; PAR2; paired-like homeodomain transcription factor 2; PITX2; klotho; KL; patched A; patched B; PTCHA; PTCHB; syndecan 1; syndecan 4; SDC1; SDC4; patched A; patched B; PTCHA; PTCHB; syndecan 1; syndecan 4; SDC1; SDC4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inhibit the expression of human Cellular Inhibitor of Apoptosis-1 (c-IAP-1). The antisense compounds may be used for diagnostics, therapeutics (for modulating the expression of c-IAP-1), prophylax: (e.g. to prevent or delay infection, inflammation, or tumor format: a research reagents (e.g. to distinguish between members of a biological pathway) and in kits. Sequences AAZ22150-189 represent phosphorothicate oligonucleotides used for antisense inhibition of cellular inhibitor of apoptosis-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
Homo sapie
                                                                                                                                                                Human; T-type calcium channel; CACNAIG; cytosine methylation; CpG island; cellular proliferative disorder; colorectal cancer; age related disease;
                          Homo sapiens
                                                         chromosome 5q; PCR primer; ss.
                                                                                                                                                                                                              Human IQGAP2 CpG island 5'-bisulfite PCR primer.
                                                                                                                                                                                                                                                                                                        AAS01590 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18 BP; 3 A; 2 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antisense compounds complementary to Cellular Inhibitor of useful for e.g. diagnostics, therapeutics, and as research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-561047/47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cellular Inhibitor of c-IAP-1; prophylaxis;
                                                                                                                                                                                                                                            18-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 15; Column 38; 32pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human c-IAP-1 mRNA inhibiting antisense oligo ISIS #23344
                                                                                                                                                                                                                                                                                                                                                                                                    160 aaatataaataaaa 173
                                                                                                                                                                                                                                                                                                                                      18
                                                                                                                                                                                                                                                                                                                                                                                 18 AAATATAAATAAAA 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention provides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cowsert LM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Apoptosis-1; antisense; infection; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antisense compounds of 8-30 nucleotides that
                                                                                                                                                                                                                                                                                                        22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ackermann EJ
                                                                                                                                                                                                                                                                                                          ВΡ
                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 14; DB 20;
Pred. No. 6.9e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnostic; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tumor formation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 18
                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prophylaxis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      reagents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Apoptosis-1
                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               formation),
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WO200119845-A1

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RESULT 19
AASO1643/c
ID AASO16
XX AASO16
AC AASO16
XX AASO16
XX BT 18-JUL
XX Human;
KW Human;
KW Cellul
KW apolip
KW G DYCT
KW G PAR2;
KW PAR2;
KW PAR2;
KW PAR2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transformed cells, CACNAIG is implicated in cellular proliferative coldisorders e.g. leukaemia, colorectal, lung, breast and other cancers. The nucleic acid coding for CACNAIG is useful as a marker for screening concer and age related diseases. A diagnostic kit containing primers (CASO1574-AASO1623) for amplification of a CpG-containing nucleic acid, where the primer hybridises with a target polynucleotide sequence (CASO1677-AASO1673), can be used for detecting aberrant methylation. The CC cpG island sequences (AASO1677-AASO1672) are selected from genes encoding CC CACNAIG, apolipoprotein B (APOB), caudal type homeobox transcription factor 2 (CDX2), epidermal growth factor receptor (EGFR), fibrillin-1 (CC (HSN1), G protein-coupled receptor 37 (GPR37), heat shock 70kD protein 6 (HSP70B: HSPA6), RasGAP-related protein (IGGAP2), klotho (KL), CC (HSP70B: HSPA6), RasGAP-related protein (HSPA6), RasGAP-related pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                         cellular proliferative disorder; colorectal cancer; age related disease; apolloporotein B; APOB; caudal type homeobox transcription factor 2; CDX2; epidermal growth factor receptor; EGFR; fibrillin-1; FBN1; G protein-coupled receptor 37; GPR37; heat shock 70kD protein 6; HSP70B'; HSPA6; RasGAP-related protein; IGGAP2; proteinase-activated receptor 2; PAR2; paired-like homeodomain transcription factor 2; PITX2; klotcho; KL; patched A; patched B; PTCHA; PTCHB; syndecan 1; syndecan 4; SDC1; SDC4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACNAIG gene correlate with several cancerous phenotypes involving various tissue and cell types. Since aberrant methylation of normally unmethylated CpG islands is often observed in immortalised and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        maps to chromosome 5q. The methylation state of specific regions within CpG islands associated with a novel T-type calcium channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid molecule for use as a marker for screening cancer, comprises the coding region for a {\tt T-type} calcium channel and regulatory sequences associated with the channel -
                                                                                                                                                                                                                    Human; T-type calcium channel; CACNAIG; cytosine methylation; CpG island;
                                                                                                                                                                                                                                                                          Human IQGAP2 5'-target sequence for bisulfite PCR.
                                                                                                                                                                                                                                                                                                                                    18-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                          AAS01643
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAS01643 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              196 ttatttttatttta 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 ttatttttattta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21; Page 34; 125pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence for 5'-bisulfite PCR primer is used to study the state of human RasGAP-related protein (IQGAP2) which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000WO-US25479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 A; 0 C; 3 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.3%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                      PTCHB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 14;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 22;
6.8e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 22;
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RESULT 20
AAV07952/c
ID AAV079
XX
AC AAV079
XY
C
AC AAV079
XX
C
AC AAV079
XX
DE Helicc
XX
GHPO 1
KW GHPO 1
KW therag
XX
Synthe
OS Synthe
OS Helicc

02-FEB-1999 AAV07952

(first entry)

AAV07952 standard; DNA;

26

ВP

Helicobacter pylori polypeptide

GHPO 1414 5'

DNA primer

Helicobacter pylori

Synthetic therapy; GHPO 1414;

PCR;

primer;

gastritis; ulcer;
ss.

vaccine;

diagnosis;

infection;

밁

21

TTATTTTTATTTA

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                                                                                                                                         Matches
                                                                 Query Match
Best Local :
                                                                                                                                                                                    cellular proliferative disorders e.g. leukaemia, colorectal, lung, brea and other cancers. The nucleic acid coding for CACNAIG is useful as a marker for screening cancer and age related diseases. A diagnostic kit containing primers (AASO1574-AASO1623) for amplification of a CpG-containing nucleic acid, where the primer hybridises with a target polynucleotide sequence (AASO1627-AASO1676), can be used for detecting aberrant methylation. The CpG island sequences (AASO1677-AASO1692) are selected from genes encoding CACNAIG, apollpoprotein B (APOB), caudal type homeobox transcription factor 2 (CDX2), epidermal growth factor receptor (EGFR), fibrillin-1 (FBNI), G protein-coupled receptor 37 (GPR37), heat shock 70kD protein 6 (HSP70B', HSPA6), IOGAP2, klotho (KL proteinase-activated receptor 2 (PAR2), paired-like homeodomain transcription factor 2 (PITX2), patred-like homeodomain
                                                                                                                                                                                                                                                                                                                                                                                                                              5'-target sequence (complementary to the 5'-bisulfite PCR primer) is used to study the methylation state of IQGAP2 which maps to chromosome 5q. The methylation state of specific regions within CPG islands associated with a novel T-type calcium channel CACNAIG gene correlate with several cancerous phenotypes involving various tissue and cell types. Since aberrant methylation of normally unmethylated CPG islands is often observed in immortalised and transformed cells, CACNAIG is implicated in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid molecule for use as a marker for screening cancer, comprises the coding region for a \mathbb{T}-type calcium channel and regulatory sequences associated with the channel -
                                                                                                                                       Sequence
                                                                                                                                                                             syndecan 1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence for human RasGAP-related protein (IQGAP2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; Page 37; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-SEP-1999;
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196 ttatttttatttta
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                                                  14;
                                                                   Similarity
                                                                                                                                       22 BP;
                                                  Conservative
                                                                                                                                                                             4 (SDC1;
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                                                                                                                                       15
                                                                                                                                       Ą; 3 С;
                                                                 100.0%;
                                                                                                                                       0 G;
                                                 0;
                                                                 Score 14;
Pred. No.
                                                                                                                                                                             or a
                                                                                                                                       4 T;
                                                  Mismatches
                                                                                                                                                                             MINT31
                                                                                                                                       0 other;
                                                                 DB 22;
6.8e+03;
                                                                                                                                                                           sequence
                                                                                    22;
                                                  0;
                                                                                 Length 22
                                                  Indels
                                                 0
                                                                                                                                                                                                                                  klotho (KL),
                                                                                                                                                                                                                                                                                                                                                                                                               lung, breast
                                                 Gaps
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RESULT 21
AAV07922/c
ID AAV07922 standard; DNA;
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Best Local
                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                               This 5' primer is used with a 3' primer (see AAV07954) in the PCR amplification of Helicobacter, e.g. Helicobacter pylori, genomic DNA in order to obtain DNA (see AAV07921) the unprocessed form of a 76 kDa polypeptide (see AAW73032) designated GHPO 1414. The isolated polypucleotide, and encoded polypeptide, can be used to develop vaccines for the treatment and prevention of Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
        Al-Garawi
                          (INMR ) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS ET VACCINS.
                                                     01-APR-1997;
01-APR-1997;
                                                                                  31-MAR-1998;
                                                                                                    08-OCT-1998.
                                                                                                                      WO9843479-A1
                                                                                                                                         Helicobacter
                                                                                                                                                                                                Helicobacter
                                                                                                                                                                                                                   02-FEB-1999
                                                                                                                                                                                                                                      AAV07922;
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 5; Page 145; 184pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated Helicobacter polynucleotides - used to
for the diagnosis, prevention and treatment of Helic
infections and gastroduodenal diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Al-Garawi A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ( HUMA - )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1997;
01-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAR-1998;
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                                                                                                                                                                                                                                                                                                              307 ttttcatgttttct
                                                                                                                                                                                                                                                                                                     18
                                                                                                                                                                    primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1998-568251/48
                                                                                                                                                                             386; infection;
                                                                                                                                                                                                                                                                                                     TTTTCATGTTTTCT
                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MERIEUX ORAVAX PASTEUR MERIEUX SERUMS ET VACCINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                       BP;
                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                        pylori
                                                                                                                                                                                             pylori
                                                                                                                                                                                                                  (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kleanthous
        Kleanthous
                                                     97US-0834666.
97US-0831310.
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97US-0831310
                                                                                  98WO-US06421
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                                                                                                                                                                                                                                                                                                                                                                                       14 A;
                                                                                                                                                                                                                                                                                                     տ
                                                                                                                                                                                                                                                                                                                       320
                                                                                                                                                                                              polypeptide GHPO 386 5' DNA primer.
                                                                                                                                                                                                                 entry)
                                                                                                                                                                                                                                                                                                                                                  4.3%;
100.0%;
                                                                                                                                                                            gastritis;
                                                                                                                                                                                                                                                                                                                                                                                       5 C;
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        Ħ,
                                                                                                                                                                                                                                                       ВP
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Pred. No.
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        Lissolo
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                                                                                                                                                                              ulcer;
                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                              vaccine;
                                                                                                                                                                                                                                                                                                                                                                                       other;
                                                                                                                                                                                                                                                                                                                                                 DB 19; 1
6.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Miller C,
        Miller
                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicobacter
        c,
                                                                                                                                                                            diagnosis; therapy;
                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                        0;
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RESULT 22
AAV07937/c
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Best Local Similarity
Matches 14; Conserv
          This 5' primer is used with a 3' primer (see AAV07939) in the PCR amplification of Helicobacter, e.g. Helicobacter pylori, genomic DNA in order to obtain DNA (see AAV07916) encoding the unprocessed form of a 76 kDa polypeptide (see AAV073027) designated GHPO 896. The isolated polynucleotide, and encoded polypeptide, can be used
                                                                                                           New isolated Helicobacter polynucleotides - for the diagnosis, prevention and treatment infections and gastroduodenal diseases
                                                                                                                                                                                                                                                   01-APR-1997;
01-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This 5' primer is used with a 3' primer (see AAV07924) in the amplification of Helicobacter, e.g. Helicobacter pylori, genom DNA in order to obtain DNA (see AAV72001) encoding the unprocessed
                                                                                      Claim 5;
                                                                                                                                                                                      Al-Garawi A,
                                                                                                                                                                                                                                                                                                                  08-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                          Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV07937 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastroduodenal diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-568251/48.
                                                                                                                                                              WPI; 1998-568251/48
                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC.
(INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS ET VACCINS
                                                                                                                                                                                                                                                                                         31-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                 Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                      therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                 GHPO 896; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV07937;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                form of a 76 kDa polypeptide (see AAW73022) designated GHPO 386. isolated polynucleotide, and encoded polypeptide, can be used to develop vaccines for the treatment and prevention of Helicobacte:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             307 ttttcatgttttct 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 TTTTCATGTTTTCT 7
develop vaccines
                                                                                    Page 141; 184pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                      PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                 pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                         pylori polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first
                                                                                                                                                                                        Kleanthous H,
                                                                                                                                                                                                                                                                                                                                                                                                     primer;
                                                                                                                                                                                                                                                  97US-0834666
97US-0831310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                 gastritis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; 4
 the treatment and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G;
                                                                                                                                                                                        Lissolo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 14;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          GHPO 896 5'
                                                                                                                                                                                                                                                                                                                                                                                                                 ulcer;
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                                                                                                                        leotides - used to develop products treatment of Helicobacter
                                                                                                                                                                                      Ļ
                                                                                                                                                                                                                                                                                                                                                                                                                 vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 19;
. 6.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             other;
                                                                                                                                                                                        Miller
 prevention of Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA primer.
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                                                                                                                                                                                      C,
                                                                                                                                                                                                                                                                                                                                                                                                                 diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of Helicobacter
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genomic
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QΥ
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                        Query Match
Best Local S
Matches 14
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2655/c
AAT42655 standard; DNA; 29 BP
                                                                                                                                                                         Compositions containing neutralising antitoxin against one or more E. coli verotoxin (VT) can be used to treat intoxicated adults and children with enteric bacterial infections. They may also be used as prophylactics e.g. as a vaccine, against diarrhoeal disease or the development of extra-intestinal complications of E.coli infection, especially haemolytic uraemic syndrome. The antitoxin can also be used to detect E. coli VT in a sample. The VT is recombinant, preferably a fusion protein containing a non-VT protein sequence and part of the E.coli VTI or VT2 sequence. Two primers (AAT42655) were used to amplify the verotoxin VT-1 A subunit coding
                                                                                                                sequence and add a histidine tag coding sequence to the subunit sequence. Two primers (AAT42655, AAT42658) were used to amplify the verotoxin VT-1 A and B subunits and add a histidine tag coding sequence to the subunit sequences.
                                                                                                                                                                                                                                                                                                                                                                           Compsn. contg. neutralising antitoxin against E.coli vero-toxin used to treat intoxicated individuals, and as a prophylactic aga diarrhoeal disease or extra-intestinal complications of E.coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Verotoxin; haemolytic
                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                   Example 6; Page 58; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carroll
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primer for amplifying verotoxin (VT-1) subunit A coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT42655
                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-505779/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (OPHI-) OPHIDIAN PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9630043-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infections
189 aaaataattattt 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      307 ttttcatgttttct 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTTCATGTTTTCT
                          l Similarity
14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                              29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             uraemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli; enteric infection; diarrhoea; vaccine; uraemic syndrome; detection; ss.
                                                                                              BP;
                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP; 14 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Padhye NV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95US-0410058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96WO-US04093
                                                                                             11 A; 2 C; 5 G; 11 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.3%; Suc. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Mismatches
                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; 4 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stafford
                           0;
                        Score 14; DB 17;
Pred. No. 6.6e+03;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 19; 1
. 6.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 27;
                                                   Length 29;
                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                           against
                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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AAA51200/c
ID AAA512
XX
AC AAA512
AC AAA512
AC AAA512
DT 26-SEP
DE N-term
XX VT-1;
KW VT-1;
KW VT-1;
KW PI NO SESCHER
OS Synthe
PN US6080
PD 27-JUN
PF 13-MAF
XX (OPHI-
XX (OPHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E. coli verotoxin (VT) type 1 and 2 subunits A and B were cloned into CC pET-23b, designed to allow expression of the native proteins containing CC c-terminal polyhistidine tags. The VT-1 and VT-2 genes were engineered CC to convert the signal sequence methionine codon into a NdeI site to convert the signal sequence methionine codon into a NdeI site to CC end convert the signal sequence methionine codon into a NdeI site to CC entroided amino acids. The C-terminal primers comprises the CC c-terminal T codons of each gene fused to the sequence CTCGAGCC, in order to add the polyhistidine tag. The primers delete the native stop codons, CC and when cloned into pET-23 add a C-terminal attension of Leu-Glu-(His)6. CC and when cloned into pET-23 add a C-terminal extension of Leu-Glu-(His)6. CC tag facilitates single step affinity purification of subunits from CC periplasmic extracts. However, due to poor recovery of his-tagged VT-1 A chains, expression of maltose binding protein (MBP) fused control to control to control to control to the total type of the VT-2 B subunit.
                                                                                                                                                                                                        claimed. The vector is chosen from pET24hisVT2BL+, pET24hisVT2BL- and pET24VT2B, where "L+" indicates that the vector encodes the preprotein form of the protein and "L-" indicates that the vector encodes the mature form of the protein. The bacterial cell is capable of expressing large quantities (40 mg/l) of VT-2B. The toxins are useful for immunizing non-mammals and for detecting bacterial toxins in environmental samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           strict uninduced promoter control is necessary to permit cell viability. Bacterial host cells expressing a recombinant expression vector encoding a polyhistidine affinity tag and a polyhistidine aff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacterial cell for recombinantly expressing bacterial toxins in large quantities useful for immunization and treatment of bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  recombinant production; so primer; polyhistidine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA51200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA51200 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 6; Column 83; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-451195/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VT-1; verotoxin; antitoxin therapy; fusion protein; affinity tag;
recombinant production; screening; dairy; anti-bacterial; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (OPHI-) OPHIDIAN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-JUN-2000
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                                                                                                              including soil, wat
obtained from food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           primer for E. coli verotoxin 1 subunit A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            userul for immunization and treatment of bacterial comprises expression vector encoding bacterial toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-0410058
                                                                                                         water, industrial samples, biological samples and samples ood and dairy processing instruments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97US-0816977
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                                                                                                                                                                                                                                                                                                                                                                       the mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 food;
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Query Match Best Local Similarity

4.3%; 100.0%;

Score 14; Pred. No.

DB 21; 6.6e+03;

Length

Sequence

29

BP; 11 A; 2 C; 5 G; 11 T; 0 other;

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RESULT 25
AAT25703/c
                                                                                                                                                                                                                     A single-stranded DNA (or its complementary strand or the corresp. C double-stranded DNA) which comprises one of the 7837 "GS" sequences given in AAT19001-T26837 and which is able to hybridise to part of human genomic DNA, CDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the G'-end of mRNA by using poly(T) as the sole primer. Since the 3'-c untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for diagn
                                                                                                                                                                                              Sequence 31 BP; 14 A; 3 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 1910; 2245pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1995-206931/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matsubara K, Okubo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09514772-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene signature; messenger RNA; mRNA; relative abundance; human; cloning; mapping; non-biased library; diagnosis; cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human gene signature HUMGS07904.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT25703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT25703 standard; cDNA to mRNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying gene signatures in 3'-directed human cDNA library -for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (OKUB/) OKUBO
                                                                 198 atttttattttaaa 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MATS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189
                                                                                                                        Local Similarity
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                                  20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aaaataattatttt 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MATSUBARA K.
                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                        100.0%;
                                                                                                                                          4.3%;
                                                                                                                                                                                            3 G; 10 T; 1 other;
                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                        Score 14;
Pred. No.
                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ω
                                                                                                                        DB 16; 1
. 6.6e+03;
                                                                                                        0,:
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                                                                                                                                       Length 31;
                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; frequency;
detection;
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                                                                                                      0;
                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e.g.
                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                                                Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                            XDX
                                                                                                                                                                                              AAZ27689/c
                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                 Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV67854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid segment comprising one of the 10 - 100 bp sequences given in the specification (sequences of a polymorphic site), or the complement of the segment and a method of analysing a nucleic acid comprising determining the base occupying the polymorphic site of the polymorphic fragment sequences are disclosed in the specification. The information obtained from nucleic acid analysis by the method described is useful in diagnosis or monitoring of diseases like cancer, inflammation, heart disease, CNS diseases, and susceptibility to infection by microorganisms. In addition, the nucleic acid segments are useful in manufacturing medication in the treatment of prophylaxis of diseases, and also the use of the DNA segments as pharmaceutical.
Synthetic
                                                                                                        22-DEC-1999
                                                                                                                                          AAZ27689
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid segments containing polymorphic sites, complements and methods of detecting a nucleic acid - fuse including diagnosis and monitoring of diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-MAR-1997;
07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleotide fragment containing polymorphic site, WI-11163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV67854;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV67854 standard; DNA;
                                Verotoxin;
                                                                   PCR primer
                                                                                                                                                                           AAZ27689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 25; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-495419/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Berno A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AFFY-) AFFYMETRIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09838846-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-DEC-1998
                                                                                                                                                                                                                                                                                                  209 aaatttgttaaaaa 222
                                                                                                                                                                                                                                                                 17 aaatttgttaaaaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polymorphic site;
er; inflammation;
                                                                                                                                                                                                                                                                                                                                     l Similarity
14; Conser
                                                                                                                                                                           standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                           31 BP; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chee M,
                                VT1;
                                                                   for Verotoxin gene
                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0042125.
97US-0813159.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-US04571
                                VT2; detection; PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fan
                                                                                                                                                                                                                                                                                                                                                                                                                         A; 2 C; 4 G; 7 T;
                                                                                                                                                                                                                                                                                                                                                  4.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid analysis; diagnosis; monitoring; heart disease; CNS disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J,
                                                                                                                                                                           32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31 BP
                                                                                                                                                                           ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lipshutz RJ;
                                                                                                                                                                                                                                                                                                                                                   Score 14;
Pred. No.
                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                           1 other;
                                                                                                                                                                                                                                                                                                                                   DB 19; I
. 6.6e+03;
ches 0;
                                                                                                                                                                                                                                                                                                                                                                    Length 31;

    for general

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PSX TTAX
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AAT97603/c
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                     Delta-virG delta-stxA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents a PCR primer of the invention. The primer is used for amplification of the E. coli verotoxin (VT) gene. The oligonucleotide is useful for detection of inactivated VT gene by transfer of a foreign DNA fragment. Simple, rapid and specific amplification of VT gene from environmental factors is achieved using oligonucleotide of the invention.
Example 6; Page 57; 94pp; English
                             Shigella mutants with mutation
                                                                                                           09-APR-1996;
                                                                                                                              09-APR-1997;
                                                                                                                                                  16-OCT-1997
                                                                                                                                                                     W09737685-A1
                                                                                                                                                                                         Shigella dysenteriae
                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                   Shigella dysenteriae delta-stxA allele PCR primer
                                                                                                                                                                                                                                                                        30-APR-1998
                                                                                                                                                                                                                                                                                            AAT97603;
                                                                                                                                                                                                                                                                                                              AAT97603 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        An oligonucleotide for amplification of verotoxin - useful in the detection of inactivated verotoxin gene by transfer of a foreign DNA
                                                                    Levine MM,
                                                                                       (UYMA-) UNIV MARYLAND BALTIMORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-603716/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JP11243996-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                           189 aaaataattatttt 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-SEP-1999.
                                                                                                                                                                                                                                                                                                                                                                17 AAAATAATTATTTT 4
                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                       32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 9;
                                                                                                                                                                                                                     allele;
allele;
                                                                   Noriega
                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP; 12 A; 2 C; 4 G; 14 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                       (first entry)
                                                                                                           96US-0629600.
                                                                                                                              97WO-US05954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98JP-0047677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98JP-0047677.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10pp; Japanese
                                                                                                                                                                                                                     delta-guaB-A allele; PCR; amplification; primer;
shigellosis; vaccine; ss.
                                                                                                                                                                                                                                                                                                               DNA;
                                                                     FR
                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                          4.3%;
                                                                                                                                                                                                                                                                                                              36
                                                                                                                                                                                                                                                                                                              ВP
                                                                                                                                                                                                                                                                                                                                                                                                     Score 14; DB; Pred. No. 6.6
                                                                                                                                                                                                                                                                                                                                                                                                      0;
                            in guaB-A -
                                                                                                                                                                                                                                                                                                                                                                                                             DB 20; I
6.6e+03;
                            used
                             ij
                                                                                                                                                                                                                                                                                                                                                                                                                       Length 32;
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                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                            vaccines against
                                                                                                                                                                                                                                                                                                                                                                                                      0;
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RESULT 29
AAC90606
ID AAC906
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Best Local
                                                                                                                         02-MAY-1991;
14-APR-1993;
26-OCT-1993;
27-JUL-1994;
03-NOV-1989;
05-DEC-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This is a PCR primer used in the amplification of the Shigella dysenteriae 1 delta-stxA allele. The delta-stxA allele was integrated into delta-guab-A of delta-guab-A, delta-virG S. dysenteriae 1, which inactivated the shiga toxin of this strain. The mutant can be used in the preparation of vaccines such as, a live vector vaccine comprising a Shigella mutant, (which encodes and expresses a foreign antigen, and a pharmaceutically acceptable carrier) or a DNA mediated vaccine comprising the Shigella mutant (which also contains a plasmid which encodes and expresses a foreign antigen in a eukaryotic cell). The vaccines can be used against Shigellosis.
                                                                   Peters D, (Goldbach RW;
                                                                                                                                                                                                        26-NOV-1996;
                                                                                                                                                                                                                               21-NOV-2000
                                                                                                                                                                                                                                                      US6150585-A
                                                                                                                                                                                                                                                                                                  misc_binding
                                                                                                                                                                                                                                                                                                                                     misc_binding
                                                                                                                                                                                                                                                                                                                                                                      misc_binding
                                                                                                                                                                                                                                                                                                                                                                                                         Tomato spotted wilt virus
                                                                                                                                                                                                                                                                                                                                                                                                                              Tospovirus resistance; transgenic plant; Impatiens necrotic spot virus; TSWV; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tomato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC90606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC90606 standard; RNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 36 BP; 11 A; 3 C; 10 G; 12 T; 0 other;
                                                                                                  (NOVS.) NOVARTIS FINANCE CORP.
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|||||||||||||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 AAAATAATTATTTT 14
                                            2001-060031/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               spotted wilt virus S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                              Gielen JJL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                        91US-0694734.

93US-0047346.

93US-0143397.

94US-0280903.

89US-0431259.

89US-0446024.
                                                                                                                                                                                                        96US-0757011
                                                                                                                                                                                                                                                                                                   /bound_moiety= 32..36
                                                                                                                                                                                                                                                                                                                                     /bound_moiety=
15..28
                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                           /bound_moiety=
                                                                                                                                                                                                                                                                                       /*tag=
                                                                                                                                                                                                                                                                                                                         /*tag=
                                                                                                                                                                                                                                                                                                                                                            /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36
                                                                                                                                                                                                                                                                                                                           σ
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                                                                                                                                                                                                                                                                                       O
                                                                              De Haan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNA partial sequence #10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 14;
Pred. No.
                                                                                                                                                                                                                                                                           "binds nucleotides
                                                                                                                                                                                                                                                                                                              "binds nucleotides
                                                                                                                                                                                                                                                                                                                                                "binds nucleotides 33-21 of AAC89655"
                                                                              γT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                              Van Grinsven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 18;
6.5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                          tomato spotted wilt virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                              19-6
                                                                              MQJM,
                                                                                                                                                                                                                                                                           5-1 of AAC89655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                              of AAC89655'
                                                                            Kool
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                              ĄJ;
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Recombinant DNA construct comprising a DNA sequence encoding an RNA sequence that codes for a tospovirus protein, useful for producing plants with reduced susceptibility to tospovirus infection -

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RESULT 3
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                                                     Query Match
Best Local
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Best Local
                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides DNA constructs encoding RNA sequences a tospovirus which can be used to produce transgenic plants with immu to tospoviruses. Examples of tospoviruses include the tomato spotted virus and the Impatiens necrotic spot virus
                                                                                                                PCR primers given in AAQ62951-52 were used to clone anti-glycophorin antibody 1C3 Fab coding region. The DNA sequence of the first 1443 bases of the Fab fragment in pHFA, ready for ligation post PCR amplification for ligation into p569, is given in AAQ62958.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycophorin; antibody 1C3; target binding polypeptide; PCR; polymerase chain reaction; primer; antibody engineering; humanized antibody; phagemid pHFA; plasmid p569;ss.
                                                                                                Sequence
                                                                                                                                                                           Example; Page 36; 67pp; English.
                                                                                                                                                                                                specificity,
                                                                                                                                                                                                         New target-binding polypeptide(s) used for diagnosis, etc. -
having a stable core polypeptide region with at least one
target-binding region covalently attached, opt. mutated to alter
                                                                                                                                                                                                                                                      WPI; 1994-135515/16
                                                                                                                                                                                                                                                                           Lah M,
                                                                                                                                                                                                                                                                                                         (CSIR ) COMMONWEALTH SCI & IND RES
                                                                                                                                                                                                                                                                                                                               25-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                     24-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                          14-APR-1994.
                                                                                                                                                                                                                                                                                                                                                                                               WO9407921-A
                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycophorin antibody 1C3 Fab coding region PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ62952 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 ttatttttattta
                     83 aaatttataattat 96
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                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30
7 uuauuuuuauuuua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 3; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Fig 16C;
                                                                                                37 BP; 14 A;
                                                                                                                                                                                                                                                                                    Colman PM,
                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP; 7
                                                                                                                                                                                                etc.
                                                                                                                                                                                                                                                                                                                                92AU-0004973
                                                                                                                                                                                                                                                                                                                                                     93WO-AU00491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; 0
                                                                                                                                                                                                                                                                           Power BE;
                                       4.3%; but
100.0%; Pr
0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            209
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                                                                                                5 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; 0 G; 29 U;
                                                                                                                                                                                                                                                                                     Hudson PJ,
                                                                                                0 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВP
                                                     Score 14;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 14; I
Pred. No. 6.
                                             Mismatches
                                                                                                 18
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                                                                                                Τ;
                                                                                                                                                                                                                                                                                                          ORG.
                                                                                                                                                                                                                                                                                    Irving
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                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22;
6.5e+03;
                                                     DB 15; I
6.5e+03;
                                                                                                 other;
                                                                                                                                                                                                                                                                                     RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                            0;
                                                               Length
                                                                                                                                                                                                                                                                                     Kortt A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                            Indels
                                                                 37;
                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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tted wilt
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DЪ
                                                                                                                                                                                                                                                                                RESULT 31
AAF55449/c
ID AAF55449 standard; DNA;
                                                                                                                                                                                                                                                                                                                                 EIB sequences, but having at least the E2B and/or E4 sequences encoding products essential for adenoviral replication. Compared with previous vectors, the new recombinant vectors are replication defective and capress the remaining viral genes only at background levels. The vector itself does not dominantly elicit a response of the immune system, but the immune response is directed primarily against the transgene product, and is less toxic to the cells which, in turn, results in a prolonged synthesis of the protein of interest. The recombinant adenoviral vectors are used in the functional characterization of gene products in vivo, and for overexpression of known and novel genes in cells lines, tissues or animals in order to find genes that encode for proteins with a desired function such as those that interfere with cell proliferation and differentiation. The vectors are further used as captage of the provide sharpsy, and for protein production in mammalian cells. Oligonucleotides AAF55449-50 were annealed together, and used to construct a shuttle vector which was used in the method of the invention.
                                                                                                                        Query Match
Best Local S
Matches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The specification describes a method for producing a recombinant adenovirus-like gene delivery vehicle having reduced expression of adenoviral E2B and/or E4 gene products in a target cell. The method comprises generating a recombinant adenoviral vector lacking E1A and comprises generating a recombinant adenoviral vector lacking E1A and comprises generating a recombinant adenoviral vector lacking E1A and comprises generating a recombinant adenoviral vector lacking E1A and comprises generating a recombinant adenoviral vector lacking E1A and comprises generating a recombinant adenoviral vector lacking E1A and comprises generating a recombinant adenoviral vector lacking E1A and comprises generating a recombinant adenoviral vector lacking E1A and comprises generating a recombinant adenoviral vector lacking E1A and comprises generating a recombinant adenoviral vector lacking E1A and comprises generating a recombinant adenoviral vector lacking E1A and comprises generating a recombinant adenoviral vector lacking E1A and comprises generating a recombinant adenoviral vector lacking E1A and comprises generating a recombinant adenoviral vector lacking E1A and comprises generating a recombinant adenoviral vector lacking E1A and comprises generating a recombinant adenoviral vector lacking E1A and comprises generating a recombinant adenoviral vector lacking E1A and comprises generating E1A and compri
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide used to construct the shuttle vector pAAO-E-TATA
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                                                          79
   21
                             ctgaaaatttataa 92
CTGAAAATTTATAA
                                                                                                                        l Similarity 100
14; Conservative
                                                                                                                                                                                                                                                                                45 BP; 14 A; 5 C;
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                                                                                                                                                        Score 14;
Pred. No.
                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                19 T; 0 other;
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thes 0;
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                                                                                                                                                                                  Length 45;
                                                                                                                           Indels
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differentiation;
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ElA and
                                                                                                                           Gaps
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AAF55450 ID AAF5

32

0;

AAF55450 standard; DNA; 45

AAF55450;

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RESULT 33
AAC88874/C
ID AAC88874 standard; E
XX
AC AAC88874;
XX
DT 05-MAR-2001 (first
XX
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                                                                                                                                                                                                                                                                                                                                             adenovirus-like gene delivery wehicle having reduced expression of CC adenoviral E2B and/or E4 gene products in a target cell. The method CC comprises generating a recombinant adenoviral vector lacking E1A and CC E1B sequences, but having at least the E2B and/or E4 sequences encoding products essential for adenoviral replication. Compared with previous CC vectors, the new recombinant vectors are replication defective and CC express the remaining viral genes only at background levels. The vector itself does not dominantly elicit a response of the immune system, but the immune response is directed primarily against the transgene product, and is less toxic to the cells which, in turn, results in a prolonged CC synthesis of the protein of interest. The recombinant adenoviral CC vectors are used in the functional characterization of gene products in vivo, and for overexpression of known and novel genes in CC cells lines, tissues or animals in order to find genes that encode for proteins with a desired function such as those that interfere with cell constructs in order to find genes that encode as CC vaccines, in gene therapy, and for protein production in mammalian cells: Oligonucleotides AAF55449-50 were annealed together, and used to construct a shuttle vector which was used in the method of the invention.
                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Producing a recombinant adenovirus-like gene delivery vehicle with modified E2B or E4 functions, for gene therapy, comprises generating an adenoviral vector where E2B or E4 is under the control of a synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The specification describes a method for producing a recombinant adenovirus-like gene delivery vehicle having reduced expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                      Sequence 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (INTR-) INTROGENE BV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adenovirus vector; gene delivery vector; E2B gene; E4 gene; vaccine; replication defective virus; cell proliferation; cell differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oligonucleotide used to construct the shuttle vector paaO-E-TaTa.
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                                                                                                                                                                 14;
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                                                                                                                                                                                                                                                                                                                      BP;
                                                                                                                                                                                                                                      Conservative
                    (first entry)
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                                                                                    DNA;
                                                                                                                                                                                                                                                                                                                    A;
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                                                                                                                                                                                                                                                      100.0%;
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Pred. No.
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                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                    0 other;
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6.4e+03;
                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                    Length 45
                                                                                                                                                                                                                                    Indels
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Db
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                                                                                                                                                                                                                                                                      RESULT 34
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is a linker used in a gene delivery vehicle comprising an element of adenovirus type 35 or a functional equivalent of such an element. The element is responsible for avoiding or reducing neutralising activity against adenoviral elements by the host to which the gene is to be delivered. The vehicle can be used to deliver genes or nucleic acids of interest to host cells. Use of the delivery system efficiently transfers genetic material to a human cell without the
                                                  16-MAY-2000;
                                                                                                                                             gene therapy;
                                                                                                                                                                               Oligonucleotide TATAmin
                                                                                                                                                                                                      05-MAR-2001
                                                                                                                                                                                                                                                 AAC88875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adenovirus derived gene delivery vehicles comprising at least one element of adenovirus type 35, efficiently transfers genetic material to a human cell without the inherent problem of pre-existing immunity
                                                                                                                                                       Adenovirus type 35; Ad35; adenovirus type
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oligonucleotide TATAplus
                                                                           22-NOV-2000
                                                                                                EP1054064-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   inherent problem of pre-existing immunity, found with previous serotypes
                                                                                                                                                                                                                                                                                                                     79 ctgaaaatttataa 92
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                                                                                                                                                                                                                                                                                                                                                       14;
                                                                                                                                                                                                                                                 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                               B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 31;
                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                     2000EP-0201738.
                                                                                                                                                                                                     (first entry)
                                                                                                                                              linker; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linker; ss
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                                                                                                                                                                                                                                                                                                                                                                                                               5 C;
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                                                                                                                                                                                                                                                                                                                                                                                                               7 G;
                                                                                                                                                                                                                                                                                                                                                       0;
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Pred. No. 6.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                               19 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                        5; Ad5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Ad5; gene delivery vehicle;
                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                           Length 45;
                                                                                                                                                        gene delivery vehicle;
                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                     0;
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(INTR-) INTROGENE BY

17-MAY-1999;

99EP-0201545

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Best Local S
Matches 14
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          Claim 1;
                                map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bout
                                             Novel biallelic markers
                                                                        WPI; 2000-013267/01
                                                                                               Cohen D,
                                                                                                                                                  21-APR-1998;
23-NOV-1998;
                                                                                                                                                                                       21-APR-1999;
                                                                                                                                                                                                                 28-OCT-1999
                                                                                                                                                                                                                                        W09954500-A2
                                                                                                                                                                                                                                                                                           variation
                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                         diagnosis; single
                                                                                                                                                                                                                                                                                                                                                                   Human genome; biallelic marker; high density disequilibrium map; genomic map; haplotype; phenotype; polymorphic base; genotyping; haplotyping; hybridisation; identification; characterisation;
                                                                                                                                                                                                                                                                                                                                                                                                                    Human map-related biallelic marker SEQ ID NO:713
                                                                                                                                                                                                                                                                                                                                                                                                                                              10-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAZ66366 standard; DNA; 47 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 45 BP; 19 A; 7 C; 5 G; 14 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adenovirus derived gene delivery vehicles comprising at least one element of adenovirus type 35, efficiently transfers genetic material
                                                                                                                        (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a human cell without the inherent problem of pre-existing immunity
                                of the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ctgaaaatttataa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ctgaaaatttataa
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       Page 382; 2745pp;
                                                                                               Blumenfeld
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 31; 138pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.3%; Solarity 100.0%; 1
Conservative 0;
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                                                                                                                                                  98US-0082614
98US-0109732
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                                                                                                                                                                                                                                                                                           replace(24,C)
                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                 /standard_name= "single nucleotide polymorphism"
                                                                                                                                                                                                                                                                                                                                                       nucleotide polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42
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                                             used to
                                                                                                 Chumakov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 14;
Pred. No.
                                               construct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22; I
6.4e+03;
                                             a high density
                                                                                                                                                                                                                                                                                                                                                         SNP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45
                                             disequilibrium
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RESULT 3
AAZ67473/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAZ65654 to AAZ69578 represent human biallelic markers from the present invention, which contain a polymorphic base at position 24 of their nucleotide sequences. AAZ69579 to AAZ77440 represent amplification primers for the biallelic markers. The biallelic markers of the invention have a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and diagnostic methods, as well as the characterisation of the differential efficacious responses to and side effects from pharmaceutical agents acting on a disease as well as other
                                                                                                                                                                                                                                                                                                                                                                           haplotyping;
diagnosis; s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              473/c
AAZ67473 standard; DNA; 47
                                   Claim 1;
                                                           Novel biallelic markers
map of the human genome
                                                                                                WPI; 2000-013267/01
                                                                                                                                                                           21-APR-1998;
23-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                 Human genome; genomic map;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Human map-related biallelic marker SEQ ID NO:1820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, and 3367, are not actually given a sequence
                                                                                                                                                 (GEST )
                                                                                                                                                                                                                21-APR-1999;
                                                                                                                                                                                                                                         28-OCT-1999
                                                                                                                                                                                                                                                                  WO9954500-A2
                                                                                                                                                                                                                                                                                                                   variation
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                                   Page 618;
                                                                                                                        Blumenfeld
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                                                                                                                                                                           98US-0082614.
98US-0109732.
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                                                                       a high density disequilibrium
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AAZ65654 to AAZ69578 represent human biallelic invention, which contain a polymorphic base at

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Best Local
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AAZ65654 to AAZ69578 represent human biallelic markers from the present invention, which contain a polymorphic base at position 24 of their nucleotide sequences. AAZ69579 to AAZ77440 represent amplification primers for the biallelic markers. The biallelic markers of the
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human genome; biallelic marker; high density disequilibrium map; genomic map; haplotype; phenotype; polymorphic base; genotyping; haplotyping; hybridisation; identification; characterisation; diagnosis; single nucleotide polymorphism; SNP; ds.
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23-NOV-1998;
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replace(24,C)
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6.4e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human genome; biallelic marker; high density disequilibrium map; genomic map; haplotype; phenotype; polymorphic base; genotyping; haplotyping; hybridisation; identification; characterisation; diagnosis; single nucleotide polymorphism; SNP; ds.
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                                                                                                                                                                    Claim 1;
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23-NOV-1998;
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                                                                                                                                                               Page 635; 2745pp;
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AAZ65654 to AAZ69578 represent human biallelic markers from the pre-invention, which contain a polymorphic base at position 24 of their nucleotide sequences. AAZ69579 to AAZ74040 represent amplification primers for the biallelic markers. The biallelic markers of the invention have a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and

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AAZ67813
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primers for the biallelic markers. The biallelic markers of the invention have a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also
                                                                                                    AAZ65654 to AAZ69578 represent human biallelic markers from the present invention, which contain a polymorphic base at position 24 of their nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                21-APR-1998;
23-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              haplotyping studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and diagnostic methods, as well as the characterisation of the differential efficacious responses to and side
                                                                                                                                                                                                    Claim 1;
                                                                                                                                                                                                                                             map of the human genome
                                                                                                                                                                                                                                                                  Novel biallelic markers used to construct a high density disequilibrium
                                                                                                                                                                                                                                                                                                                                                         Cohen D,
                                                                                                                                                                                                                                                                                                                                                                                                    (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             variation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosis; single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human map-related biallelic marker SEQ ID NO:2160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ67813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ67813 standard; DNA;
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                                                                                                                                                                                                  Page 691; 2745pp;
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                                                                                                                                                                                                                                                                                                                                                           Blumenfeld M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         biallelic marker; high density disequilibrium map; haplotype; phenotype; polymorphic base; genotyping; hybridisation; identification; characterisation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pharmaceutical agents acting on a disease
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98US-0109732
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Pred. No.
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6.4e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence Listing
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Best Local Similarity
                                                                chosen absolute number of variations. (A), and analysis of their sequences, are useful for the following: (i) determining a predisposition to disease, especially colorectal, endometrial and ovarian carcinoma and leukemia; (ii) determining an increased mutation rate (frequency of base substitutions, insertions and/or deletions) in eukaryotic cells; (iii) predicting the progression, severity and survival time of patients with neoplastic disease; (iv) the development of therapeutic and 'life-style'
                                                                                                                                                                                                   This invention describes a novel method of determining a predisposition to disease by genotyping a subject's DNA sequence (A) of the human mismatch repair gene, MSH6 at specified positions and comparing with
                        drugs; (v) predicting individual differences in response to known chemotherapeutic agents (e.g. cis-platin) or drugs developed from (iv); (vi) optimizing individual treatments and interventions against
                                                                                                                                                                      reference DNA sequences, optionally taking into account all possible combinations of variations of the individual mutations, including an
                                                                                                                                                                                                                                                                                     Novel variants of the human mismatch repair gene, MSH6, useful e.g. determining predisposition to cancer and for development of drugs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pharmaceutical agents and diagnostic methods, as well as the characterisation of the differential efficacious responses effects from pharmaceutical agents acting on a disease as verificated agents.
                                                                                                                                                                                                                                                                                                                                                                Plaschke J,
                                                                                                                                                                                                                                                                                                                                                                                                                          06-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mutation; carcinoma; colorectal; endometrial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human MSH6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neoplastic disease; drug development; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    be useful for the identification of the targets for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    198 atttttattttaaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NOS 2852, 2913, 2974, 3035, are not actually given a sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention
            (vii) controlling the mutation rate in eukaryotic cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fragment 8/exon
                                                                                                                                                                                                                                                          Fig 3; 14pp; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repair gene; hMSH6; disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19
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                                                                                                                                                                                                                                                                                                                                                                Schackert
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ovarian; leukemia;
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AAF48097
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               of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBp]-2 or IGFBP], which is capable of inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF45151 and AAF45153-F45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, runa, pilaris, serborrhoea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the such as a neovascular condition of the skin, a hyperneovascular condition such as a neovascular condition of the such a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neovascular condition of the retina; ss.
                                                                                                                                                                                                                                                                                          The present invention relates to a method for ameliorating the effects
                                                                                                                                                                                                                                                                                                                                                                                        proliferation and/or
                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                              Ameliorating the effects of a disorder, e.g. psoriasis, b administering UV (ultra-violet) treatment (optional) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         development of pharmaceuticals; (ix) developing diagnostic kits and other systems for genotyping; and (x) developing in vivo and in vitro test systems for expressing individual forms of the MSH6 gene, e.g. for studying pathophysiology of disease or processes in which MSH6 is involved, and for drug development and testing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MURD-) MURDOCH CHILDRENS RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antisense therapy;
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brain or skin, growth factor-mediated malignancies,
                                                                                                                                                                                                                                                                                                                                                                                                            tering UV (ultra-violet) treatment (optional) and an a acid that inhibits or reduces growth factor mediated
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                                      inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF45151 and AAF45153-F45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other
                                                                                                                                                                         The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation,
                                                                                                                                                                                                                                                                                                                         Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an a nucleic acid that inhibits or reduces growth factor mediated
                           sclerotic disease, kidney disease, hyperproliferation of the inside of
                                                                                                                                                                                                                                                                              Example 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilar growth factor mediated cell proliferation; ichthyosis; serborrhoea; keratosis; neoplasia; sclerodermae; wart; skin cancer; sclerotto disentyperneovascular condition; hyperplasia; kidney disease;
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                                                                                                                                                                                                                                                                              Page 54;
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                                                                                                                                                                                                                                                                                                                                         receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF45151 and AAF45153-F45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, neeplasias, scleroderma, warts, benign growths, cancers of the trian abundance of the process of the p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
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                                                                                                                                 skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood vessels or any other buscase.
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Sequence 15
                                                                                                             blood vessels or any other hyperplasia
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                                                                                                                                           50 kilobases in length. The complex also comprises one or more polypeptides selected from a cell recognition domain, a protein transduction domain, a protein degradation domain, an intracellular targeting domain, a protein interaction domain, an epitope domain and a protein purification domain. The complexes are used to deliver a nucleic acid to a cell. The nucleic acids delivered are of various sizes and preferably greater than 50 kilobases, especially more than 100 or more than 200 kilobases in length.
                                                                                                                                                                                                                                                  AAA57752-66 represent sequences which are bound by the Z2 domain of the human RIF60 polypeptide. RIF60 is a zinc finger protein. The nucleic acid binding domain of the RIF60 polypeptide is used to construct a non-viral nucleic acid delivery complex comprising a modular polypeptide. The complex comprises a modular peptide containing a nucleic acid binding domain and a nucleic acid condensation domain that bind with and condense a nucleic acid molecules.
                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                        molecule into a cell comprises a modular polypeptide
                                                                                                                                                                                                                                                                                                                                                                                            Non-viral nucleic acid delivery complex for delivering a nucleic molecule into a cell comprises a modular polypeptide .
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XX Conciferase; enzyme; bioluminescenc entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This 17-mer oligonucleotide DNA probe, along with Probe-2 (AAQ92085) are used to screen an R. reniformis cDNA library to isolate cDNA encoding Renilla luciferase. The luciferase was then expressed using E. coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New recombinant Renilla luciferase polypeptide - used as a luminescent tag, partic in bio-luminescence assays and for the prodn of antibodies
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                                                                                                                                                                                           Renilla reniformis luciferase DNA probe-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               January 24, 2002, 02:22:17; Search time 216.42 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
/SIDS2/gcgdata/geneseq/geneseqn/Na1989.DAT: *
/SIDS2/gcgdata/geneseq/geneseqn/Na1990.DAT: *
/SIDS2/gcgdata/geneseq/geneseqn/Na1990.DAT: *
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/SIDS2/gcgdata/geneseq/geneseqn/Na1993.DAT: *
/SIDS2/gcgdata/geneseq/geneseqn/Na1993.DAT: *
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/SIDS2/gcgdata/geneseq/geneseqn/Na2000.DAT: *
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                                                                                                                                                                                                                                                                                                                                                                                                                                               /SIDS2/gcgdata/geneseq/geneseqn/NA1980.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqn/NA1984.DAT:*
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356.526 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1861242
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

, , , 2	; ō	Score	Match	Match Length DB	DB	Ħ	Description
	Н	90	100.0	1392	20	AAX60299	DNA encoding the b
	N	60	66.7	327	20	AAX60300	Promoter of the
O	ω	32.6	36.2	9542	20	AAX20260	Borrelia burqdorfe
C	4	32.4	36.0	4015	22	AAS01490	Human secreted
C	Çī	31.6	35.1	6250	21	AAA62306	Caenorhabditis ele
C	σ	31.2	34.7	3337	17	AAT34620	P. vivax ESP-1
C	7	31.2	34.7	3337	20	AAX15174	DNA encoding a
C	œ	31.2	34.7	3337	22	AAH76457	Plasmodium vivax E
	9	30.8	34.2	1226	21	AAC35351	Arabidopsis thalia
C	10	30.8	34.2	13830	22	AAD02659	Tomato chromosome
a	11	30.6	34.0	936	22	AAF58252	Oligonucleotide D1

Clostridium beta2 toxin gene promoter and signal sequence - useful against toxins from Clostridium perfringens

Example A; Page 31; 46pp; French.

Gibert M, Popoff MR

(INSP) INST PASTEUR.

WPI; 1999-217498/19.

P-PSDB; AAY16591

	G	C				C			C					ဂ	O	a										O			C	C	ဂ	C	ဂ	C
	45	44	43	42	41	40	39	38	37	36	35	34	<u>υ</u>	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12
	29.4	•	29.4	•	•	•	•												29.8				39	30	30	•	•	•		•	•	•	30.6	
	•	•	•		•		•	•	32.9		•		•		•	•	•		33.1	•	•	•		ω		•				4.	4.	4.	34.0	4 .
	1978	1405	1223	1222	1219	546	393	110000	5994	1703	1703	1703	1703	1592	1518	513445	14426	14417	3454	784	324	210	4140	244	9.0	2364	134	87350	692	938	936	.936	936	936
	22	22	21	21	21	2 2	21	22	21	22	22	19	12	21	17	22	22	22	22	22	20	20	18	22	20	21	20	18	20	22	22	22	22	22
,	AAH14169	AAH34185	AAC40150	AAC45059	AAC48516	AAH09430	AAC09962	AAF84800	AAA70222	AAF23618	AAD04541	AAV15701	AAQ15131	AAZ97085	AAT37313	AAI61373	AAI62921	AAI62923	AAH18466	AAH05038	AAX61491	AAX61492	AAT77331	AAF58238	_AAX60301	AAA70246	AAX13328	AAX83003	218	AAF58255	AAF58262	AAF58259	AAF58257	AAF58254
	Human cDNA sequenc			thal	Arabidopsis thalia	cDNA clor	Human secreted pro		um fa			ni ACC	CC1 en	u.	Aromatic acyl tran	Soybean 318013 reg	Human genomic DNA		CDNA	Human cDNA clone (burgdorferi	B. burgdorferi ant	Solanum tuberosum		Eragment of the be	Plasmodium falcipa	0		— -				Oligonucleotide D1	Oligonucleotide D1

ALIGNMENTS

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19-SEP-1997;
                                                                                                                                                       Clostridium perfringens.
                                                                                         19-SEP-1997;
                                                                                                                                                                                                           12-AUG-1999 (first entry)
                                                                                                                                                                                                                                           AAX60299
                                                                                                                                                                      vaccine; Clostridium tetani;
                                                                                                                                                                             Beta-2 toxin; Clostridium perfringens type C; gene promoter;
                                                                                                                                                                                            DNA encoding the beta-2 toxin of Clostridium perfringens type
                                                                                                                        26-MAR-1999.
                                                                                                                                        FR2768747-A1.
                                                                                                                                                                                                                             AAX60299;
                                                                                                                                                                                                                                           standard; DNA; 1392 BP.
                                                                                         97FR-0011710.
                                                                                                         97FR-0011710.
                                                                                                                                                                      SS
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O

XSSSSSSSXXX

The present sequence encodes the beta-2 toxin of Clostridium perfringens type C. The specification describes the Clostridium perfringens beta 2 toxin gene promoter (see AAX60300). The sequences can be used to produce vaccines against Clostridium, and especially Clostridium perfringens, or Clostridium

Query Match Matches

Local Similarity

100.0%; ilarity 100.0%; Conservative (

0;

Mismatches

Indels

0

Gaps

0;

Score 90; DB 20; Pred. No. 9.9e-13;

Length 1392;

Sequence 1392

BP;

606 A; 115 C;

209 G;

462 T; 0 other;

terant

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RESULT
AAX60300
ID AAX6
XX AAX6
XX AAX6
XX Prom
XX Beta
XX Vacc
XX Clos
XX Clos
XX Clos
XX I9-5
PN FR27
XX I9-5
PR 19-5
XX INE
XX INE
XX CLOS
XX INE
XX INE
XX CLOS
XX
                                QΥ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
                                                                                                                                                 Query Match
                                                                                           Matches
                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                 The present sequence represents the promoter of the beta-2 toxin gene of Clostridium perfringens type C. The beta2-toxin promoter and gene sequences can be used to produce vaccines against Clostradium especially Clostridium perfringens, or Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clostridium beta2 toxin gene promoter and signal sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gibert M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FR2768747-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Beta-2 toxin; Clostridium perfringens type C; gene promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAX60300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX60300 standard; DNA; 327 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             against toxins from Clostridium perfringens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-217498/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Promoter of the beta-2 toxin gene of Clostridium perfringens type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            268
                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
1 atgaaaaaattatttcaaagtttactgtaatttttatgtttccatgttttcttattgtt 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 atgaaaaaaattatttcaaagtttactgtaatttttatgttttcatgttttcttattgtt 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         atgaaaaaaattatttcaaagtttactgtaatttttatgttttcatgttttcttattgtt 327
                                                                                                                                                                                                                                          327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 32; 46pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clostridium tetani;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Popoff MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        perfringens
                                                                                           Conservative
                                                                                                                                                                                                                                          BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97FR-0011710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97FR-0011710
                                                                                                                                                                                                                                       141 A; 13 C;
                                                                                                                      66.7%;
100.0%;
                                                                                           0;
                                                                                                                   Score 60;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SS
                                                                                                                                                                                                                                    44 G; 129
                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              357
                                                                                     8.7e-06;
hes 0;
                                                                                                                                                                                                                                    T; 0 other;
                                                                                                                                                 DB 20;
                                                                                                                                              Length 327;
                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                    Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        usetul
                                                                                        0;
                                                                                     Gaps
                                                                                        0;
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RESULT 4
AAS01490/c
ID AAS014

AAS01490 standard; DNA; 4015

ВP

DЬ δÃ 밁

3872

GAACTATTTATAATAAAAAGGAGAGCA 3846 gcaataagtccaatgaaagcaagtgca

64

3932 AAAATAAACATAGCTAAATTAATTTTATATTAATATTTCATTATTTGTAATATCTTGT 3873

0,

90

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RESULT 3
AAX20260/c
                                                                                                            Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Вþ
                                                    Query Match
Best Local S
                                         Matches
                                                                                                                                              AAX20248 to AAX20402 represent polynucleotide sequences isolated from Borrelia burgdorferi (Bb). Products derived from Bb can be used for the detection, diagnosis, characterisation, prevention and therapy of Bb infections, e.g. Lyme disease. They can also be used for the production of biosynthetic products, e.g. enzymes. Borrelia belongs to a family of motile, spiral-shaped bacteria called Spirochetes. Spirochetes are pathogenic in humans and Borrelia causes epidemic and endemic relapsing fever, and Lyme borreliosis, more commonly known as
                                                                                                                                                                                                                                                                           Claim 1; Page 920-925; 1128pp;
                                                                                                                                                                                                                                                                                                   New isolated Borrelia burgdorferi nucleic acids - used tproducts for the detection, diagnosis, characterisation, and therapy of infections, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                   Clayton R,
                                                                                                                                                                                                                                                                                                                                                                                                                                ( HUMA - )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme epidemic relapsing fever; endemic relapsing fever; Lyme borr infection; diagnosis; characterisation; detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAX20260 standard; DNA; 9542
                                                                                                            Sequence 9542 BP; 3812 A; 1160 C; 1113 G; 3457 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-081217/07.
                                                                                                                                                                                                                                                                                                                                                                                        White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-JUL-1997;
22-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-SEP-1997; .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-DEC-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9858943-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAX20260;
                                                                                                                                      Lyme disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          268 atgaaaaaattatttcaaagtttactgtaatttttatgttttcatgttttcttattgtt 327
                                                      Local Similarity
4 aaaaaaattatttcaaagtttactgtaatttttatgttttcatgttttcttattgttgga 63
                                                                                                                                                                                                                                                                                                                                                                                                                                HUMAN GENOME SCI INC
MEDIMMUNE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          burgdorferi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       burgdorferi
                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    Dougherty BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97US-0057483.
97US-0050359.
97US-0053344.
97US-0053377.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-US12764.
                                                    36.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polynucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                    Fraser C,
                                        0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΒP
                                                    Score 32.6;
Pred. No. 22;
                                                                                                                                                                                                                                                                           English.
                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    Lathigra R,
                                                                    DΒ
                                        34;
                                                                   20;
                                                                 Length 9542;
                                                                                                                                                                                                                                                                                                                                 used to
                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                    Smith HO;
                                                                                                                                                                                                                                                                                                                    prevention
                                                                                                                                                                                                                                                                                                                                   develop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                reliosis;
                                      0;
                                        Gaps
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                                 Qy
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                                                                                                                  Qy
                                                                                                                                                                                                                                                             CC invention relates to 43 novel human secreted proteins (AMU01040)-AMU01082)
CC and their gene sequences which can be used in gene therapy. The secreted condition or useful to prevent, treat or ameliorate a medical condition condition or susceptibility to a pathological condition. Antibodies to condition or susceptibility to a pathological condition. Antibodies to condition or susceptibility to a pathological condition. Antibodies to condition or susceptibility to a pathological condition. Antibodies to condition or susceptibility to a pathological condition. Antibodies to condition or susceptibility to a pathological condition. Antibodies to condition or susceptibility to a pathological condition antibodies to condition or susceptibility to a pathological condition. Antibodies to condition or susceptibility to a pathological condition. Antibodies to condition or susceptibility to a pathological condition. Antibodies to condition or susceptibility to a pathological condition. Antibodies to condition or susceptible conditions associated conditions and disorders which are diagnosed conditions or suspenditions or system disorders e.g. cardiac arrest, cerebrovascular disorders e.g. conditions caused by bacteria, viruses and fungi and coular disorders e.g. corneal infection. The polypeptides can also be condition or suspendition, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities.
                                                                                                                                                            Matches
                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hyperproliferative disorder; cardiovascular disorder; cerebrovascular disorder; nervous system disorder; infection; ocular disorder; wound healing; epithelial cell proliferation; skin aging; transplantation; tissue regeneration; chemotaxis;
                                                                              3088
3028 GAGCTA 3023
                                                                                                                                                                                                                                                           Sequence 4015 BP; 1122 A; 712 C; 743 G; 1438 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAS01460-AAS01502 encode for novel human secreted proteins. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 452-453; 516pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding 43 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-266138/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-SEP-2000; 2000WO-US26376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-APR-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human secreted protein; gene therapy; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS01490;
                                      62
                                                                                                                      N
                           gagcaa 67
                                                                                                 tgaaaaaaattatttcaaagtttactgtaatttttatgttttcatgttttctttattgttg 61
                                                                            TGAGAAAAGGTTATTGAAAAGTTACAGTCATTTGTATTCTTTCATTTCTCATGTTAGTTG 3029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             additive; preservative; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU01070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ruben SM,
                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0155808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein gene #31.
                                                                                                                                                                               36.0%;
68.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Komatsoulis GA;
                                                                                                                                                                             Score 32.4;
Pred. No. 24;
                                                                                                                                                            Mismatches
                                                                                                                                                                                                DB 22;
                                                                                                                                                          21;
                                                                                                                                                                                              Length 4015;
                                                                                                                                                          Indels
                                                                                                                                                          0;
                                                                                                                                                        Gaps
                                                                                                                                                          0,
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RESULT 5
AAA62306/c
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                                                                                                                                                   Query Match
Best Local
                                                                                                                                      Matches
                                                                                                                                                                                                                                                                  homology to mammalian PDK. A number of C. elegans genes have been identified as homologues of genes in the mammalian insulin signalling pathway. The C. elegans age-1 gene encodes a homologue of the mammalian PI 3-kinase whilst daf-2 encodes a homologue of the mammalian receptor. The C. elegans AKT kinase and PKB kinase act downstream of daf-2 and age-1, just as their mammalian homologues act downstream of insulin signalling. The C. elegans PTEN lipid phosphatase homologue, DAF-18, has been found to act upstream of AKT in the pathway. This discovery has enabled mammalian PTEN action to be mapped to the insulin signalling pathway. Conserved DAF motifs can be used to design probes to identify mammalian DAF homologues and thus to identify individuals with a predisposition toward the development of glucose intolerance
                                                                                                                                                                                                                                                                                                                                                                                                                                                             elegans. It encodes two are homology to mammalian PDK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Diagnosing and treating obesity and impaired glucose tolerance using modulators of daf-18 expression and/or activity - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA62306 standard; DNA; 6250
                                                                                                                                                                                                                        Sequence 6250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 35; 402pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAB06177, AAB06178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200033068-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            insulin signalling pathway; daf-2; age-1; insulin receptor; PI 3-kinase; PKB kinase; PTEN lipid phosphatase; antidiabetic; anorectic; obesity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans; pdk-lb; AKT kinase; daf-18; insulin rinsulin signalling pathway; daf-2; age-1; insulin r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans pdk-1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA62306
                                                                                                                                                                                                                                                          conditions, such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-JUN-2000
                                                                 793 GTAAAATGTGAAAAAAA 776
                             64 gcaataagtccaatgaaa
                                                                                   4 aaaaaaattatttcaaagtttactgtaatttttatgttttcatgttttccttattgttgga 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000-423022/36
                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ent sequence is the genomic sequence of pdk-1 from Caenorhabditis
It encodes two alternatively spliced isoforms which shows
to mammalian PDK. A number of C. elegans genes have been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                      Conservative
                                                                                                                                                                                                                          BP; 1972 A; 1225 C; 1140 G; 1913 T; 0 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0205658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US28529
                                                                                                                                                                                                                                                        as obesity and diabetes.
                                                                                                                                                     35.1%;
                              81
                                                                                                                                      0,
                                                                                                                                                   Score 31.6;
Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВP
                                                                                                                                      Mismatches
                                                                                                                                                                     DB
                                                                                                                                      29;
                                                                                                                                                                     Length
                                                                                                                                                                       6250;
                                                                                                                                  0
                                                                                                                                  Gaps
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RESULT 6 AAT34620/c

0

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RESULT 7
AAX15174/c
ID AAX15174 standard; DNA; 3337 BP
                                                                             ρy
                                                                                                      В
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                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                         The present sequence encodes a species-specific Plasmodium vivax malarial antigen, PVESP-1. The gene appears to be missing a small portion of its 5' end. This protein is secreted into the plasma of a susceptible mammalian host after infection. Monoclonal/polyclonal antibodies can be utilised in assays used to diagnose malaria, as well as to determine whether P. vivax is the species responsible for the
                                                                                                                                                                                                          Sequence 3337 BP; 1304 A; 467 C; 875 G; 691 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                  Antibodies to Plasmodium vivax blood stage antigens - used to diagnose malaria and to determine whether P. vivax is the speresponsible for infection
                                                                                                                                                                                                                                                                                                                                                                                                                                 Barnwell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P. vivax ESP-1 blood stage antigen coding sequence
                                                                                                                                                                                                                                                                                                                           Example 4; Column 15-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYNY ) UNIV NEW YORK STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US5532133-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ESP-1; blood stage antigen;
causative agent; antibody; r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT34620 standard;
                                                                                                      138
                                                         78
                                                                              70
                                                                                                                           10
                                                                                                                                                              Local Similarity
                                                                              agtccaatgaaagcaa 85
                                                                                                                 attatttcaaagtttactgtaatttttatgttttcatgttttcttattgttggagcaata 69
                                                                                                                                                                                                                                                                                                                                                                                               1996-321110/32.
DB; AAR98747.
                                                         ATTAAAAGAAAAGCAA 63
                                                                                                     AATATATGTATATAGCAGTTTTTATAGATTATTTTTATCTTACTGTTGAAGCATGA 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vivax (clone PvMB3.3.1).
                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93US-0072610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9305-0072610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence
231..3197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92..230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note- "contains typical malaria intervening
    sequence splice sites splice sites"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA;
                                                                                                                                                             34.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "encodes initial (N-terminal) sequence of
hydrophobic amino acids"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        o
                                                                                                                                                                                                                                                                                                                          22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    monoclonal;
                                                                                                                                                  0,
                                                                                                                                                             Score 31.2;
Pred. No. 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВÞ
                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 malaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polyclonal; assay;
                                                                                                                                                                         DΒ
                                                                                                                                                                         17;
                                                                                                                                                 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 infection;
                                                                                                                                                                       Length
                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                            the species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ds
                                                                                                                                                 0;
                                                                                                                                                Gaps
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                   QY
                                             Вb
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                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                         02-JUN-1993;
07-JUN-1995;
30-SEP-1996;
                                                                                                                                                                                      The protein comprises an epitope not present in other Plasmodium species that cause malaria in humans, and is bound by monoclonal antibody 1011G10. The peptide antigen can be used in immunoassays for diagnosis of malaria caused by P. vivax and/or can be used to produce antibodies
                                                                                                                                                                                                                                     The present sequence encodes a C-terminal erythrocyte secreted protein-1 (pvESP-1) of Plasmodium vivax. PvESP-1 is a malarial antigen which is a secreted blood-stage protein present in detectable amounts in biological samples from individuals infected with P. vivax.
                                                                                                                                                    Sequence 3337 BP; 1304 A; 467 C; 875 G; 691
                                                                                                                                                                                                                                                                                                                                   Plasmodium vivax peptide antigen -
                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-180063/15
P-PSDB; AAW97039.
                                                                                                                                                                                                                                                                                                                                                                                             Barnwell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exon
                                                                                                                                                                                                                                                                                                Example 4; Fig 5A-C; 23pp; English.
                                                                                                                                                                                                                                                                                                                        by Plasmodium vivax
                                                                                                                                                                                                                                                                                                                                                                                                                   (UYNY ) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US5874527-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium viyax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Erythrocyte secreted protein-1; PvESP-1; malarial antigen;
blood-stage protein; malaria; monoclonal antibody 1D11G10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX15174;
                                             138
78
                      70
                                                                                          Local Similarity
mes 48; Conserv
                                                                                                                                                                            use in such immunoassays.
                                                        attatttcaaagtttactgtaatttttatgttttcatgttttcttattgttgtagcaata 69
                      agtccaatgaaagcaa
 ATTAAAAGAAAAGCAA
                                             AATATATATGTATATAGCAGTTTTTATAGATTATTTTTATCTTACTGTTGAAGCATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein;
                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a secreted blood-stage protein called PvESP-1
                                                                                                                                                                                                                                                                                                                                                                                                                    NEW YORK STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                         93US-0072610.
95US-0478417.
96US-0719822.
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/number= 1
231..3194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /number=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92..230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1..91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /number= 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "contains 1 intron"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= b
                                                                                                      34.7%;
63.2%;
                      85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ۵
                                                                                          0;
                                                                                                        Pred.
                                                                                                                 Score
                                                                                           Mismatches
                                                                                                      31.2;
No. 4
                                                                                                                                                                                                                                                                                                                                   for diagnosis
                                                                                                        44;
                                                                                                                 DВ
                                                                                                                                                    Τ;
                                                                                          28;
                                                                                                                 20;
                                                                                                                                                       0
                                                                                                                                                     other;
                                                                                                                                                                                                                                                                                                                                    of malaria caused
                                                                                                                Length
                                                                                           Indels
                                                                                                                 3337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ds
                                                                                          0;
                                                                                          Gaps
                                               79
                                                                                          0;
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RESULT 8
AAH76457/C
ID AAH764
                          Query Match
Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                    02-JUN-1993;
07-JUN-1995;
30-SEP-1996;
                                                                                                                    The invention relates to novel species-specific Plasmodium vivax malarial peptide antigens which are proteins or fragments of proteins secreted into the plasma of a susceptible mammalian host after infection, and to monoclonal or polyclonal antibodies directed against those antigens. The peptide antigens, monoclonal antibodies, and/or polyclonal antibodies are useful in assays to diagnose malaria, and to determine which P. vivax species is responsible for the infection. The present sequence encodes P. vivax erythrocyte secreted protein-1 (PESP-1), a secreted species-specific blood stage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exon
                                                                                     Sequence 3337 BP; 1304 A; 467 C; 875
                                                                                                           antigen provided in the invention.
                                                                                                                                                                                                                                            Example 4; Fig 5; 23pp; English.
                                                                                                                                                                                                                                                                             New species-specific Plasmodium vivax malarial peptide antigens, proteins or fragments secreted into the plasma of susceptible mammalian
                                                                                                                                                                                                                                                                                                                    P-PSDB;
                                                                                                                                                                                                                                                                                                                                                       Barnwell JW;
                                                                                                                                                                                                                                                                                                                                                                             (UYNY ) UNIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US6231861-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium vivax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium vivax;
species-specific;
malaria; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium vivax ESP-1 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH76457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH76457 standard; DNA; 3337 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      intron
  10 attatttcaaagtttactgtaatttttatgttttcatgttttcttattgttgtagcaata 69
                                                                                                                                                                                                                                                                   after infection, useful for
                                                                                                                                                                                                                                                                                                                    2001-335068/35.
DB; AAG66528.
                           Conservative
                                                                                                                                                                                                                                                                                                                                                                             NEW YORK STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                    93US-0072610.
95US-0478417.
96US-0719822.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0092458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /number= 1
92..230
/*tag= c
/number= 1
231..3197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ′*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ESP-1; erythrocyte secreted protein-1; PvESP-1; malarial peptide antigen; infection; diagnosis;
                                     34.7%;
63.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "ESP-1"
                           0,
                                      Score 31.2;
Pred. No. 44;
                           Mismatches
                                                                                                                                                                                                                                                                  diagnosing malaria
                                                                                     G; 691 T;
                                                  DB
                          28;
                                                  22;
                                                                                     0
                                                                                     other;
                                               Length 3337;
                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PvESP-1;
                          0;
                          0,
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AAC35351
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                                   14 - MAY - 1999

18 - MAY 1999

19 - MAY 1999

20 - MAY - 1999

21 - MAY 1999

22 - MAY 1999

25 - MAY 1999

27 - MAY 1999

01 - JUN - 1999

03 - JUN - 1999

07 - JUN - 1999

07 - JUN - 1999

08 - JUN - 1999
                                                                                                                                                                                                     06-MAY-1999;
07-MAY-1999;
11-MAY-1999;
14-MAY-1999;
14-MAY-1999;
14-MAY-1999;
                                                                                                                                                                                                                                                                              04-MAY-1999;
05-MAY-1999;
06-MAY-1999;
                                                                                                                                                                                                                                                                                                                  30-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                            06-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-FEB-1999;
05-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAC35351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000EP-0301439
99US-0136782.
99US-0137522.
99US-0137502.
99US-0137502.
99US-0137724.
99US-0138094.
99US-0138847.
99US-0138847.
                                                                                                          99US-0135124.
99US-0135353.
99US-0135629.
99US-0136021.
99US-0136392.
                                                                                                                                                                     99US-0134370.
99US-0134768.
99US-0134941.
                                                                                                                                                                                                                                                     99US-0132484.
99US-0132485.
99US-0132486.
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99US-0132863.
                                                                                                                                                                                                       99US-0134218.
99US-0134218.
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99US-0134221.
                                                                                                                                                                                                                                                                                                                99US-0130891.
99US-0131449.
99US-0132048.
99US-0132407.
                                                                                                                                                                                                                                                                                                                                                                                                               99US-0127462.
99US-0128234.
99US-0128714.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0123548
99US-0125788
                                                                                                                                                                                                                                                                                                                                                                99US-0130449
99US-0130510
                                                                                                                                                                                                                                                                                                                                                                                                    99US-0129845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0123180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0121825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85
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AATATATATGTATATAGCAGTTTTTATAGATTATTTTTATCTTACTGTTGAAGCATGA 79
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Arabidopsis thaliana DNA fragment
                                                                      AAC35351 standard; DNA; 1226
                                                                      ВР
 SEQ
 ID
 NO:
 9873
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Hybridisation assay; genetic mapping; gene expression protein identification; signal transduction pathway; matabolic mathway; promoter; termination sequence; s gene expression control;

δÃ

 $\left(\left(Y_{t}\right) \right) _{t=0}^{2}$

16-JUN-1999; 16-JUN-1999; 17-JUN-1999;

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20-AUG-1999
20-AUG-1999
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23-AUG-1999
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27-AUG-1999
27-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-AUG-1999
13-AUG-1999
13-AUG-1999
16-AUG-1999
17-AUG-1999
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20-AUG-1999
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20-AUG-1999
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25-AUG-1999
                           990S-0148341
990S-0148541
990S-0148563
990S-014968
990S-0149922
990S-0149922
990S-0151065
990S-0151066
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990S-0151266
990S-0156458
990S-0156458
990S-0156458
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990S-0156656
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990S-0156666
990S-01561666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       $-0150884

$-0151065

$-0151086

$-0151303

$-0151303

$-0151438

$-0151930

$-0152363

$-0152363

$-01539758

$-01539758
 DB
Length
 1226;
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990S-0139452
990S-0139453
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990S-0139456
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990S-0144834
990S-0144335
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990S-0146386
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990S-0147303

18-JUN 1999
19-JUN 1999
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27-JUN 1999
27-JUN 1999
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28-JUN 1999
29-JUN 1999
20-JUN
0;

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RESULT 10
AAD02659/c
D AAD02659 standard; DNA; 13830 BP
                                                                                                 exon
                                                                                                                                                  exon
                                                                                                                                                                                                                                                                                                  exon
 exon
                                                                                                                                                                                                  exon
                                                                                                                                                                                                                                                                                                                                                                                                           CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tomato; RIN; ripening inhibitor; MC; macrocalyx; sepal development; senescence; pathogen infection; ethylene response; transgenic plant; ds.
                                                  exon
                                                                                                                                                                                                                                                   exon
                                                                                                                                                                                                                                                                                                                                                   exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tomato chromosome 5 harbouring the RIN and MC genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAD02659;
                         intron
                                                                         intron
                                                                                                                          intron
                                                                                                                                                                          intron
                                                                                                                                                                                                                          intron
                                                                                                                                                                                                                                                                          intron
                                                                                                                                                                                                                                                                                                                           intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lycopersicon esculentum
                       4433..4531

*tag= 0

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4532..4572

/*tag= p

/number= "7"
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/number= "5"
4249.4389
/*tag= m
/number= "5"
4390.4432
/*tag= n
/number= "6"
                                                                                                                                                                                                                        3835..3897

/*tag= h

/number= "3"

3898..3919
                                                                                                                                                        3924..4149
/*tag= k
/number= "4"
                                                                                                                                                                                                                                                                                396..3268

/*tag= e

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3269..3347

/*tag= f

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                                                                                                                                                                                                                                                                                                                                 211..395
/*tag= d
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                                                                                                                                                                                                                                                                                                                                                                /product= "Tomato ripening-inhibitor (RIN) protein" /note= "The specification states that the RIN gene has 9 exons and 8 introns, however the sequence represented in the figure 7 shows 10 exons and
                                                                                                                                                                                                                                                         3348..3834
/*tag= g
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                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= b
/note= "Transcribed region of RIN gene"
211..5489
                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Putative transcription start site of RIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1600..4603
                                                                                                                                                                                 *tag= j
number= "4"
                                                                                                                                                                                                         *tag= i
number= "3"
                                                                                                                                                                                                 920..3923
                                                                                                                                                 50..4248
                                                                                                                                                                                                                                                                                                                                                          introns"
                                                                                                                                                                 exon
                                                                                                                        exon
                                                                                                                                                                                                                                                                         exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exon
                                                                         exon
                                                                                                                                                                         exon
                                                                                                                                                                                                                         exon
                                                                                                                                                                                                                                                                                                                                          exon
                                                                                                                                                                                                                                                                                                                                                                                   CDS
intron
                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  promoter
                                               intron
                                                                                                intron
                                                                                                                                                                                                 intron
                                                                                                                                                                                                                                                 intron
                                                                                                                                                                                                                                                                                                                  intron
                                                                                                                                                                                                                                                                                                                                                                                                          misc_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 intron
                                                                                                                                                                                                                                             /*tag= aa
/number= "1"
8440..10594
/*tag= ab
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/note= "The rin mutation terminates within this
region of the MC gene"
10595..10671
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10672..11375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= u
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/note= "The rin n
this region"
5405..5489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= r
/number= "8"
4604..4862
/*tag= s
/number= "8"
/*tag= am
/number= "7"
12993..13449
                       /*tag= al
/number= "6"
12880..12992
                                                       12560..12600

/*tag= ak

/number= "6"
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/*tag= aj
/number= "5"
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/*tag= ai

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/*tag= ah
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                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= x
/note= "Putative transcription start site of MC"
8238..13830
                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= w
/note= "MC promoter sequence; This region separates
the RIN from the MC transcribed region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= v
/number= "10"
5695..8237
                                                                                                                                                                       11446..11686

/*tag= af

/number= "3"

11687..11785
                                                                                                                                                                                                        11376..11445
/*tag= ae
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                                                                                                                                                                                                                                                                                                                                      /product= "Tomato macrocalyx (MC) protein" /note= "The coding region has 8 exons and i y 7 introns" (251.8439
                                                                                                                                                                                                                                                                                                                                                                            /*tag= y
/note= "Transcribed region of MC
/note= "Transcribed region of MC
8251..13552
                                                                                                                                                        /*tag= ag
/number= "4"
                                                                                                                                                                                                                                 /*tag= ad
/number= "2"
                                               2601..12879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= t
'number= "9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  993..5404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         863..4992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mutation begins at a point within
                                                                                                                                                                                                                                                                                                                                                                                         gene"
                                                                                                                                                                                                                                                                                                                                                          and is interrupted
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RESULT 11
AAF58252/C
ID AAF58252 standard; DNA; 936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВĎ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of ethylene response, and DNA markers for assisted breeding. The RIN and MC genes are used in genetic transformation techniques to manipulate a variety of plant characteristics. Hence these genes represent a valuable new tool for the creation of transgenic plant preferably having one or more added beneficial characteristics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exon
                                                WO200107665-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The
01-FEB-2001.
                                                                                                   Synthetic
                                                                                                                                                                          Electron-transfer
                                                                                                                                                                                                                        Oligonucleotide D1835
                                                                                                                                                                                                                                                                           24-APR-2001
                                                                                                                                                                                                                                                                                                                        AAF58252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7128 TGAAATATTAAACCAATCTAATCTAATTCA 7099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 13830 BP; 4991 A; 1594 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genes. The invention relates to the RIN (ripening-inhibitor) and MC (macrocalyx) genes. The RIN and MC genes are useful in controlling of fruit ripening and quality, control of sepal development and size, control of senescence, control of pathogen infection, control size, control of senescence, control of pathogen infection, control size, control of senescence, control of pathogen infection, control size, control of senescence, control of pathogen infection, control size, control of senescence, control of pathogen infection, control size, control of senescence, control of pathogen infection, control size, control of senescence, control of pathogen infection, control size, control of senescence, control 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 7; 167pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid sequence comprising RIN (ripening-inhibitor) or MC (macrocalyx) genes for use in genetic transformation techniques to manipulate a variety of plant characteristics -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Giovannoni J, White R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TEXA ) UNIV TEXAS A & M SYSTEM (CORR ) CORNELL RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-JUL-2000; 2000WO-US19035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200104315-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present sequence is tomato chromosome 5 harbouring the RIN and MC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  atgaaaaaaattatttcaaaagtttactgtaatttttatgttttcatgttttcttattgtt 60
                                                                                                                                                 expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ggagcaataagtccaatgaaagcaagtgca 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-103084/11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               __ay= an
/number= "7"
13450..13552
/*tag= ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0143364.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tanksley S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= ao
/number= "8"
                                                                                                                                                                     group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.2%;
58.9%;
                                                                                                                                                                       ETM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'Vrebalov J,
                                                                                                                                                                                                                                                                                                                                                                           ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 30.8; D
Pred. No. 57;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                       mismatch;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1910 G; 5335 T; 0 other;
                                                                                                                                                                       genotyping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Padmanabhan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 13830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ٧,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ruezinsky D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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RESULT 12
AAF58254/c
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Watches 3; Conserve
                                                       DЬ
                                                                                                                                                                                                                                                                                                                                                                                 γ
                                                                                                                                                                                                                                                                                                                                                                                                          망
                                                                                                                                                                                                                                                                                                                                                                                                                             δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                  26-JUL-1999;
17-MAR-2000;
                                                                                                                              01-FEB-2001.
                                                                                                                                                                                              Electron-transfer gene expression; s
                                                                                                                                                                                                                                 Oligonucleotide D1875
                                                                                                                                                                                                                                                                               AAF58254;
                                                                                                                                                                                                                                                                                                      AAF58254 standard; DNA; 936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a single surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-159728/16
WPI; 2001-159728/16
                       Umek RM
                                                                                                     26-JUL-2000; 2000WO-US20476
                                                                                                                                                   WO200107665-A2
                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                       24-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    monitoring gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 6; Page 127; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Umek RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUL-1999;
17-MAR-2000;
                                           (CLIN-) CLINICAL MICRO SENSORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CLIN-) CLINICAL MICRO SENSORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                              396 TAAGCWWWWWWWWWWWWWWW 376
                                                                                                                                                                                                                                                                                                                                                                                                          456
                                                                                                                                                                                                                                                                                                                                                                                    61 ggagcaataagtccaatgaaa
                                                                                                                                                                                                                                                                                                                                                                                                                               1 atgaaaaaaattattcaaagtttactgtaatttttatgttttcatgttttcttattgtt 60
                                                                                                                                                                                                                                                                                                                                                                                                          936
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP; 4 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0145695
2000US-0190259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000WO-US20476
                                                                   2000US-0190259
                                                                                                                                                                                                                                                        (first entry)
                                                                                99US-0145695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression.
                                                                                                                                                                                                r group; ETM; mismatch; genotyping;
ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.0%;
3.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               139 C; 10 G; 7 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    k; Score 30.6; D
red. No. 59;
62; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     81
                                                                                                                                                                                                                                                                                                      ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               776. other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on

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AAF5827/C
ID AAF582
XX AAF582
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                                                                           acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatc) and single-nucleotide polymorphisms, e.g. for genotyping,
  Sequence 936
                                                      monitoring gene
                                                                                                                                                                 The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having
                                                                                                                                                                                                                                                  Example
                                                                                                                                                                                                                                                                                                         a single surface
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CLIN-) CLINICAL MICRO SENSORS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JUL-1999;
17-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Electron-transfer group;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other;
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                                                   single-nucleotide polymorphisms, itoring gene expression.
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3; Conserv
                                                                                                                                                                                                                                                  6; Page 127; 159pp; English.
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  BP;
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2000US-0190259.
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5 A;
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  142 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81
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Pred. No. 59;
  7 G;
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6 T; 776 other;
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Best Local Similarity
                                                                                                                                                                  The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-APR-2001
                                                                                                                                      Sequence 936 BP; 6 A; 138 C; 8 G; 8 T;
                                                                                                                                                          monitoring gene
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                                                                                                                                                                                                                                                         a single surface
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17-MAR-2000;
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376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62;
                                                                                                                                                                                                                                    English.
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RESULT

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AAF59262/c

ID AAF59262;

XC AAF59262;

XX AAF59262;

XX AAF59262;

XX 24-APR-2001 (first entry)

XX Oligonucleotide D2007.

XX Synthetic.

XX Gene expression; ss.

XX Synthetic.

XX W0200107665-A2.

XX W01500000-US20476.

XX W015000000-US20476.

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Search completed: January 24, 2002, 02:22:23 Job time: 1891 sec
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Best Local Similarity
Matches 3; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 936 BP; 5 A; 139 C; 10 G; 6 T; 776 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface \,
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gene expression; ss.
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%; Pred. No. 59;
62; Mismatches 16;
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Database :
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Maximum Match 100%
Listing first 45 summaries
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90
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Gapop 10.0 , Gapext 1.0
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987.954 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1 AX004615 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE		42 C 43 C 45	40 41		c 35		0 0 0 0 31 0		c 27	c 25		20 c 21	c 18		c 14			1 O 1		ن م	1 44- (. N H	Result No. S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           98085977
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/transl_table=11
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Bacteria; Firmicutes; Ba
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Patent: WO 9915669-A 1 01-APR-1999;
Patent: WO 9915669-A 1 01-APR-1999;
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Gibert, M. and Popoff
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NVKTEFLIKALIDMEFTYSSKOKILIVSDMEFRKVENERKYILTPSFRTQVCTWDDEL
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Pred. No. 1.9e-10;
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DEFINITION

AP003515 Clostridium

perfringens 54310 bp

DNA circular BC plasmid pCP13 DNA,

BCT

complete sequence

10-AUG-2001

LOCUS

	gene CDS	gene CDS		FEATURES SOURCE gene GDS	ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL
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CDS	gene	gene CDS	gene CDS	gene CDS	gene
/gene="PCP08" complement(58047966)	/gene="Porton" /function="ATP-binding protein" /function="ATP-binding protein" /function="ATP-binding protein) from Bacilius halodurans (213 aa); 49% identity in 214 aa overlap" /codon_start=1 /transl_table=11 /product="probable ABC transporter" /protein_id="BAB62445.1" /db_xref="GI:15076720" /translation="MNITEISNLWKKYFDKVIFKDFSLSTKKGEMIAISGRSGCGKST LLNMIGLIEKFDSGEIIIDGVKNIKINSKLANKFLREKISYLFONFALVDEETVEENL RLAIKHTIKNTKKLEEEIIRCLKEFVGLEGCGKNYIYELSGGEQGRVAIARLMLKFSEI ILADEPTGSLDEBRRDILISLKEENLSGKTIIIVTHDNYVAKQADRIIFL" complement(58047966)	/transl_table=11 /product="probable transposase" /protein_id="BAB62444.1" /db_xref="GI:15076719" /translation="MLYTTNVIESLNSQFRKFTKTKLIFPNDVSLIKMLYLATEKVNK KWTRNYPN" complement(51695804) /gene="PCP07" complement(51695804)	/COOOn_Start=1 /transl_table=11 /transl_table=11 /product="probable transposase" /product="probable transposase" /protein_id="BAB62443.1" /db_xref="GI:15076718" /translation="MISKHQRNINRIEDKNLNLYASGITTRDVAGQIKALYDIEISAE TVSNITNRIMPLYSEW" 45884746 /gene="pcp06" 45884746 /gene="pcp06" 45884746 /gene="pcp06" 658 .4746 /gene="pcp06" 45884746 /gene="pcp06" /gen	/db_xref="G1:15076717" /db_xref="G1:15076717" /translation="MSKDFLRNYIKEONFNDSNNVLNSLKDLFNDVLQEVVSAEL /translation="MSKDFLRNYIKEONFNDSNNVLNSLKDLFNDVLQEVVSAEL /translation="MSKDFLRNYIKEONFNDSNNVLNSLKDLFNDVLQEVVSAEL /dven="PCPVNSRNGYSKKTIKSELGTITLNILRYRN" 40404222 /gene="PCP05" 40404222 /gene="PCP05" /gene="PCP05" /note="60 aa, similar to gp:AF143819_1 transposase-like protein from Escherichia coli (402 aa); 38% identity in aa overlap truncated"	/codon_start=1 /transl_table=11 /transl_table=11 /product="hypothetical protein" /protein_id="BaB62440.1" /protein_id="BaB62440.1" /db_xref="GI:5076715" /db_xref="GI:5076715" /db_xref="GI:5076715" /translation="MEKILAEKRINISEYKRKNGALVTTLYLPPKWLEVIGITENERE CFFYIEDKAIKISKEKQSEEAKEKTISFSKTSTKTYLNNKWLEYLGVSEDERSCIIEL RKKDITLVKDNGRDILDI" 3773. 4024 /gene="PCP04" /gene="PCP04" /proteinid=pestis (402 aa); 44% identity in 50 aa cverlap truncated" /codon_start=1 /probable transposase" /protein_id="BaB62442.1"

/gene="PCF08"
/note="720 aa, similar to gp:AP001508_3 BH0280 gene
product from Bacillus halodurans (713 aa); 23% identity in
661 aa overlap"

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RESULT
AX004614
KEYWORDS
                                                                                    DEFINITION
                                       VERSION
                                                                ACCESSION
                                                                                                         FOCUS
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Best Local
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                                                           Sequence 2 from Patent W09915669. AX004614
                                         AX004614.1 GI:9928055
                                                                                                     AX004614
                                                                                                                                                                                                                                                                                                                                                                                               Similarity 98. 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="probable transposase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="PCP10"
8779. .9012
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WKFMLELICIYSIMIIFTIVSVLI PYITVSKITLSHIL RNKFPKSIIILNSIYVIL
ASIILLFFSNALDDLSSIGKOYKNKYWEEFROYYLL ENELGENDESIOSFSIEBEREK
ERAVYLYFNKQGAILADFNRYEPTSMEEAKQMLPEEYMRETIIVNPNYLLKHKYYDVD
GNIINISEDEKDRILLYPEKYRNFEKELLEYYGYNSQEBCSSTFCSHKYADGKLMLVE
OKOKIIMMKSNQXFSYLLDNYBEEGRYVTDPYVSVLTESNDKLVSYXYKIIGYNNSPE
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GIRANSEEEYINGLEKYYDMSVYLIDPYNLYDNVASTIINIKAKVKVIIFFAIVILLAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aa overlap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="77 aa, similar to probable transposase from
Yersinia pestis plasmid pMT1 (402 aa); 25% identity in 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8779.
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QAQSSKFYCGEQKHRATARVKVGTTLYEAKDIKDAKLTAHAQTKYYKGVTEWNSYYAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(8043.
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INIIYFTLLLVVIELVFIIFNINSLEKKNLIKVIKGEY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="conserved hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="PCP11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       truncated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="103 aa, no significant homology"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="PCP09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="PCP09"
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Pred. No. 3.9e-10;
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Savery, G.,

Scherer, S.,

Scott, G.,

Shim, C.,

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Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                           Muzny, D.M., Addams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bukay, C., Benton, J., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chiu, D., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Emerling, S., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Flagg, N., Ford, J., Hamilton, K., Han, J., Harris, C., Harris, K., Harti, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Hume, J., Ioshikhes, I., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Karatovic, J., Kureshi, A., Landry, N., Leal, B., Lee, E., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louiseged, H., Lozado, R.J., Lunsey, L., Martin, R., Martin, R.
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Clostridium perfringens
Bacteria; Firmicutes; Ba
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Gibert,M. and Popoff,M.R.
Clostridium toxin, and method for preparing
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Homo sapiens 12 BAC RP11-255114 (Roswell Park Cancer Institute
Human BAC Library) complete sequence.
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Location/Qualifiers
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Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                      Number of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANNOTATION OF FEATURES:
STSs are identified using ePCR (Genome Res. 7:541-550) searches
of a local database that includes entries from dbSTS, GDB, and
local mapping efforts.
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                                                                                                                                                                                     Average error rate (BCM·Phrap estimate): Fraction of Phrap values less than 40 :
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Submitted (19-JAN-2000) Human Genome Sequencing Center, Depar of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA
[bases 1 to 128809)
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57; Conserv
                                                                                                                                                                             Direct Submission
Submitted (10-SEP-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Sep 26, 2000 this sequence version replaced a: 100/47417
                                                                                                                  Sequencing vector: plasmid; 5% Chemistry: Dye-primer ET; 95% of reads Chemistry: Dye-terminator Big Dye; 5% of reads Assembly program: Phrap; version 0.990319 (Consensus quality: 137562 bases at least Q40 (Consensus quality: 137552 bases at least Q20 (Consensus quality: 141453 bases at least Q20)
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                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 152816)
                                                                     Insert size: 150000; agarose-fp Insert size: 149516; sum-of-contigs Quality coverage: 3.13 in Q20 bases; agarose-fp Quality coverage: 3.30 in Q20 bases; sum-of-contigs
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Waterston, R.H.
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NOTE: This is a 'working draft' sequence. It currently consists of 34 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
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114189. .123937
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                /note="assembly_name:Contig46"
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/note="assembly_name:Contig47"
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98624. .106597
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28425. .33027
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16686. .18458
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53768. .68619
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20660. .23709
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18559. .20559
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14839. .16585
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1256. .2579
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/chromosome="UNK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (26-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, Ma 02141, USA On Apr 5, 2000 this sequence version replaced gi:6759152. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55;
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Anderson, S., Baldwin, J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTG; HTGS_PHASE1; HTGS_DRAFT
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(bases 1 to 165176)
Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 157408 bases at least Q40 Consensus quality: 161068 bases at least Q30 Consensus quality: 162457 bases at least Q20 recent of the program of the progra
                                                                                                                                                                                                                                                        Center project name: L5174
Center clone name: 145_G_19
Center clone Summary Statistics
                                                                                                                                                                                                            Sequencing vector: M13; M77815; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                     Contact: sequence_submissions@genome.wi.mit.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center code: WIBR
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Pred. No. 57
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality coverage: 4.3 in Q20 bases; agarose-fp Quality coverage: 4.4 in Q20 bases; sum-of-contigs
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128302 165176: contig of 36875
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40594 522
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98573 128201: contig of 29629 bp in length
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3499 3598: gap of 100 bp
3599 6363: contig of 2765 bp in length
6364 6463: gap of 100 bp
6464 8738: contig of 2275 bp in length
8739 8838: gap of 100 bp
8839 12799: contig of 3961 bp in length
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                                                                                                                       /note="assembly_fragment"
98573. 128201
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52310. .71806
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40594. .52209
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3599. .6363
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19512. 29228
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                                        clone_end:T7
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71907. .98472
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/db_xref="taxon:9606"
/chromosome="17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       location/Qualifiers
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71806: contig of 19497 bp in length
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KEYWORDS
SOURCE
ORGANISM
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Thes 55; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Hewland, J.C., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., McTwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Beterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TACCACAAGAATCTTATAAGTCAATG 18297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (05-DEC-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 20, 2000 this sequence version replaced g1:9123832.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC016788 167322 bp DNA HTG 20-SI
Homo sapiens clone RP11-11E12, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens, clone RP11-11E12
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 167322)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 167322)
Insert size: 170000; agarose-tp
Insert size: 165922; sum-of-contigs
Quality coverage: 4.9 in Q20 bases;
Quality coverage: 5.0 in Q20 bases;
                                                                                                     Consensus quality: 159178 bases at least Q40 consensus quality: 163354 bases at least Q30 consensus quality: 164761 bases at least Q20
                                                                                                                                                                                      Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
                                                                                                                                                                                                                                                                                                    Center project name: L3141
Center clone name: 11_E_12
                                                                                                                                                                                                                                                                                                                                                   Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Whitehead Institute/ MIT Center for Genome Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www-seq.wi.mit.edu
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64.0%;
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Pred. No. 57;
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786116 86215: gap or
86216 98453: contig of 12256 -.
98454 98553: gap of 100 bp
98554 116358: contig of 17805 bp in length
116459 116458: gap of 100 bp
134094 134193: gap of 100 bp
134194 162917: contig of 28724 bp in length
162918 16317: gap of 100 bp
167322: contig of 4305 bp in length
163017: gap of 100 bp
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69482 77833: contig of 8352 bp in length
77834 77933: gap of 100 bp
77934 86115: contig of 8182 bp in length
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4428 6881: co
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728 9827: gap of 100 bp
328 12474; contig of 2647 bp in length
475 12574: gap of 100 bp
475 12574: gap of 100 bp
575 14864: contig of 2290 bp in length
865 14964: gap of 100 bp
965 18976: contig of 3912 bp in length
965 18976: gap of 100 bp
977 60052: contig of 41076 bp in length
053 60152: gap of 100 bp
053 60152: gap of 100 bp
053 60381: contig of 9229 bp in length
087 84881: ran of 100 bp
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60153. .69381
                                                                                                                                        /note="assembly_fragment"
98554. .116358
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86216. .98453
                                                                                                                                                                                                                                                         /note="assembly_fragment" 69482. .77833
                 /note="assembly_fragment"
163018. .167322
                                                         /note="assembly_fragment"
134194. .162917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP11-11E12"
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clone_end:SP6
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ORGANISM
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VERSION
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JOURNAL
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Best Local
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les 55; Conserv
                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                              preserved
                                                                                                                                                                   as soon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jaj
(E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/Tel:81-45-503-9111, Fax:81-45-503-9170)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (29-MAR-2001) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APO03462 1897/1 bp DNA HTG 30-MAR-2001 HOMO Sapiens chromosome 11 clone RP11-480C22 map 11q, WORKING DRAFT SEQUENCE, 13 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hattori,M., Ishii,K., Toyoda,A., Fujiyama,A., Yada,T., Totoki,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HOMO Sapiens DNA, clone:RP11-480C22
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  43267
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                                                                                                                                                                                                                                                                                             Sequencing vector: PCR products; 100% of reads Chemistry: Dye-terminator ET-amersham; 100% of reads Assembly program: Phrap; version 0.990329 (Consensus quality: 187154 bases at least 040 (Consensus quality: 188004 bases at least 020 (Consensus quality: 188264 bases at least 020 (Consensus quality: 188264 bases at least 020 (Consensus quality: 188264 bases at least 020 (Consensus quality: 188271; sum-of-contigs (Quality coverage: 8.56x in 020 bases; sum-of-contigs)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center project name: HumDraft11
Center clone name: RP11-480C22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center code: RIKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: RIKEN Genomic Sciences Center(GSC)
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mail: 31742 c 33143 g
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clone_end:T7
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    Project Information

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Pred. No. 57;
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Watanabe, H. and Sakaki, Y.
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43167 43266: gap of 100 bp
43267 62703: contig of 19437 bp in length
62704 62803: gap of 100 bp
62804 84476: contig of 21673 bp in length
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/note="assembly_fragment"
62804. .84476
                                                                                        /note="assembl
183262. .18584
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154017. .163781
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141582. .153916
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/db_xref="taxon:9606"
/chromosome="11"
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37254 c 36581 g 58007 t
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                                                                                  Chemistry: Dye-terminator Big Dye; 0% of reads Chemistry: Dye-terminator Big Dye; 0% of reads Chemistry: Dye-terminator Big Dye; 0% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 187074 bases at least Q40 Consensus quality: 192835 bases at least Q30 Consensus quality: 195819 bases at least Q20 Insert size: 182000; agarose-fp Insert size: 195112; sum-of-contigs Quality coverage: 7.73 in Q20 bases; sum-of-contigs Quality coverage: 7.34 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (15-JUL-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
On Aug 17, 2000 this sequence version replaced aircollian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTG 17-AUG-20 HOMO Sapiens chromosome 11 clone RP11-480C22, WORKING DRAFT SEQUENCE, 10 unordered pieces.

AC074180
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                                                                                                                                                                                                                                                                                                                                                                           Center project name: H_NH0480C22
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Waterston, R.H.
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* NOTE: This is a 'working draft' sequence. It currently * consists of 10 contigs. The true order of the pieces * is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                  Sequencing vector: M13; 2% Sequencing vector: plasmid; 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site:http://genome.wustl.edu/gsc/index.shtml
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* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will

as soon as it be preserved.

3181 3281 12432 12532

3180: 3280: 12431: 12531:

contig of 3180 bp in length gap of unknown length contig of 9151 bp in length gap of unknown length contig of 10609 bp in length

* arbitrary. Gaps between the contigs are represented as

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ALII4194.1 GI:5828813
cDNA library; nitrogen deprivation.
Botryotinia fuckeliana
Botryotinia fuckeliana
Eukaryota; Fungi; Ascomycota; Pezizor
Helotiales; Sclerotiniaceae; Botryot;
1 (bases 1 to 148)
Bitton, F., Levis, C., Fortini, D., Prac
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/note="assembly_name:Contig30
clone_end:Sp6
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96146, .124103
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/organism="Homo sapiens"

/db_xref="taxon:9606"
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124204. .160061
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35036. .50440
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12532. .23140
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34953: contig of 11995 bp in le
35035: gap of unknown length
50440: contig of 15405 bp in le
50540: gap of unknown length
71299: contig of 20759 bp in le
71399: gap of unknown length
96045: contig of 24646 bp in le
96145: gap of unknown length
124103: contig of 27958 bp in le
124103: gap of unknown length
124103: gap of unknown length
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64.0%;
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160161: gap of unknown length
193415: contig of 33254 bp in
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 Pradier, J.M.
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                     Submitted (27-MAY-1999)
                                       Direct Submission
                                                                                                 Submitted (20-OCT-1998)
                                                                                                                                                                                                                                                                                   The C. elegans Sequencing Consortium.

The C. elegans Sequencing Consortium.

Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science. 282 (5396), 2012-2018 (1998)
                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                      Waterston, R
                                                                                   University, 4444 Forest
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The CDNA library to be analyzed within the framework of this
project was created using a Botrytis cinerea strain which was grown
under conditions of nitrogen deprivation, which is the normal
situation for B. cinerea during its development on its host plant.
The library was produced in an oriented direction, in the pBSII
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/note="Genoscope sequence ID : W52A031"
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On Jan 5, 2000
Submitted by:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (09-AUG-2001) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, Louis, MO 63110, USA
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ogram Genefinder(P. Green and L. Hillier, ms in preparation)
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St. Louis , MO 63110, USA,
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8587. .8756,9042. .9167)
/gene="K07A9.2"
                                                                                                                                                                                                                                /note="C. elegans Ca2+/calmodulin-dependent protein kinase I (GB:AB021864); contains similarity to Pfam domain pr00069 (pkinase), Score=262.3, E-value=2e-75, N=1; coded for by the following C. elegans cDNAs: yk306d5.3, yk306d5.5, AB021864"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="Bristol N2"
/db_xref="taxon:6239"
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                               Louis, MO 6311
On Jun 3, 1999
Submitted by:
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Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
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Rhabditoidea; Rhabditidae; Pel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 35.4;
Pred. No. 96;
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                                                                                                                                                                    Department of Genetics, Washington Park Avenue, St. Louis, Missouri 6.
                                                                                                                                                                                                                                                     Department of Genetics, Washington Park Avenue, St. Louis, Missouri 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            and Duckels,G.
s cosmid F55A8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chromadorea; Rhabditida;
     Washington University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .10658,10709. .10810,11291. .11470,
                                                     replaced gi:3193146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31;
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                                                                                    Genetics, Washington
4444 Forest Park Ave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 33460;
                                                                                                                                                                       Missouri 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                      Avenue,
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                                                                                        St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
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Cambridge CB10 IRQ, England email: rw@nematode.wustl.ed
                                                Sanger Centre, Hinxton Hall
                                                                          St. Louis , MO
rw@nematode.wustl.edu and jes@sanger.ac.uk
                                                                     and
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neighboring submissions. NOTICE: This sequ It may be shorter E: This sequence may not be the entire insert of this clone. y be shorter because we only sequence overlapping sections or longer because we provide a small overlap between

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one ml3 subclone.

NEIGHBORING COSMID INFORMATION

The 5' clone is W03A6, 22600 bp overlap,3' clone is Y48A5B, 2100 bp overlap. Actual start of this clone is at base position 22401 of CELF55A8; actual end is at 67531 of CELF55A8.

FEATURES the Coding program Genefinder(P. Green and L. Hillier, ms in preparation). /organism="Caenorhabditis elegans" /strain="Bristol N2" Location/Qualifiers

JULII(104. .259,12869. .13036,14716. .14951,16153. .17407. .17503,23798. .23921,25619. .25726,27685. .29221. .29854,31878. .31973)
//gene="F55A8.2" /clone="F55A8" /db_xref="taxon:6239" .31973

CDS gene

/note="contains similarity to Pfam domains PF00027 (CNMP_binding, Score=246.9, E-value=9.3e-71, N=2), PF00069 (pkinase, Score=250.6, E-value=6.8e-72, N=1) and PF00043 (pkinase_C, Score=16.7, E-value=0.00024, N=1); coded for by the following C. elegans cDNAs: yk2f8.5, yk4q10.3, yk17d12.3, yk55a6.5, yk41a13.3, yk52d1.3, yk52d1.5, yk17d1.3, yk55a6.5, yk55f2.3, yk52f2.5, yk11h1.3, yk55a6.5, yk85f2.3, yk55f2.5, yk17d12.5, yk31h11.5, yk85a5.5, yk87g1.3, yk243f5.5, yk317d2.5, yk395h7.5, yk325d6.5, yk32610.5, yk343d2.5, yk49d8.5, yk385d7.5, yk479h11.5, yk486b10.5" PF00069

codon_start=1/

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> TVMGELAILYNCTRTASVQALTDVQLWVLDRSVFQMITQRLGMEHSQLNNFLTKVSI
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> EIRVLMQDFFGERALLGEEVETANIKAQAGVEVPTLDRESFGKLIGDLESLKKDYG
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> 65506. 69344
> 65506. 69346 /note="contains similarity to Pfam domains PF00027 (CNNP_binding, Score=246.9, E-value=9.3e-71, N=2), PF00069 (pkinase, Score=250.6, E-value=6.8e-72, N=1) and PF00433 (pkinase, Score=16.7, E-value=6.8e-72, N=1) coded for by the following C. elegans cDNAs: yk2f8.5, yk4g10.3, yk4g10.5, yk6b12.5, yk17d12.3, yk30f8.5, yk44la5.3, yk4g10.5, yk6b12.5, yk2f12.3, yk5563.3, yk55f2.3, yk55f2.3, yk55f2.5, yk4la5.3, yk59f31.3, yk59f31.3, yk87g1.3, yk87g1.3, yk87g1.3, yk87g1.3, yk87g1.5, yk419102.5, yk34948.5, yk243f5.5, yk295h7.5, yk317d2.5, yk349d12.5, yk349d8.5, yk385d7.5, yk395h7.5, yk410a4.5, yk443d2.5, yk469c5.5, yk486b10.5" 65506. Join(65506. .65631,65677. .66207,66728. .66964,69158. .69394) /gene="F55A8.1" /gene="F55A8.1" .69394 coded for by PF00069

CDS gene

/note="contains similarity to Pfam domain PF00320 (GATA), SCOre=42.5, E-value=3e-09, N=1; coded for by the following C. elegans cDNAs: yk99g8.5, yk115f7.5, yk330b8.5, yk330f7.5, yk3340f2.5, yk344129.5, yk345d6.5, yk390a2.5, yk404g2.5, yk446e9.5, yk4474a4.5, yk484g12.5, yk524e12.5"/codon_start=1

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TQMPTMATGGVSTDGALTMTFNLLEQGISQFTQAQELMNSSATF"

Query Match Best Local Local Similarity 39.3%; Score 35.4; Pred. No. 95; DВ ω, Length 69431;

BASE COUNT ORIGIN

21037

Matches

Conservative

0,

Ъ γ 4004 AAAAGCTTTTTGAAAATTTTCAGAAATTTTTAAATTTCCACATTTTCATTTTTTTAAGG 3945 σ aaaaattatttcaaagtttactgtaatttttatgttttcatgttttcttattgttttttattgttttcttattgtttttcttattgttttcttattgttttcttattgtt Mismatches 31; 0;

δÃ 66 aataagtccaatgaaagcaagtgca 90

밁 3944 CAGAAATTCTGGGATGCCACGTACA 3920

VERSION KEYWORDS AC006364/c LOCUS DEFINITION ACCESSION RESULT AC006364 AC006364.3 sequen Homo sapiens AC006364 132319 bp ns BAC clone GI:4753253 GS1-146J4 from 7q31.1-31.3, complete

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REFERENCE
AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (21-DEC-1999) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6. On May 5, 1999 this sequence version replaced gl:4337286.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (11-SEP-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
6 (bases 1 to 132319)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (05-MAY-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
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Waterston, R.H.
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Submitted (11-JAN-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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Ryan, E., Bauer, C., Tucci, S. a
The sequence of Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
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Sulston, J.E. and Waterston, R.
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Homo sapiens
                                                                                                                       The sequence of this clone was established as part of a mapping a sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap
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                       (http://www.genomesystems.com).
Cell line: lymphoblastoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between neighboring data submissions.
Haplotypes:
                                                               This clone is from the first BAC library from Genome Systems, Inc
                                                                                   SOURCE INFORMATION:
                                                                                                                                                                                                                                                                                         MAPPING INFORMATION:
                                                                                                                                                                                                                                                                                                                                 restriction digest.
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(bases 1 to 132319)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center project name: H_GS146J04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_famil
7983. .808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family 7930. .7982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="AT_rich"
7396. .7704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="Retroviral"
6413. .6446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="L2"
1216. .1506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="(TA)n"
8111. .8253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="(CA)n"
7359. 7395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="POLY_G" 3880. .4030
                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_f
11660.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="match to EST 10401...10850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3810.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /map="7q31.1-31.3"
/clone="GS1-146J4"
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11766. .121
                                                                                                                                                                                                                                                                                                                                                           /note="similar to Mus musculus uc72e08.y1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="GSBAC1"
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                                                                                                                               /protein_id="AAD54511.1"
/db_xref="GI:5870323"
                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10754. .11029
/note="match to EST
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                                                                                                                                                                        /product="GS3786" '
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30494. 30552.31735. 31785,34555.

44132. .44221)

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GINVALANGKTGEVLDTKYFDMWGGDVAPFIEFLKAIQDGTIVLMGTYDDGATKLNDE
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10754. .11029
ARRLIADLGSTSITNLGFRDNWVFCGGKGIKTKSPFEQHIKNNKDTNKYEGWPEVVEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST AI220397 (NID:g3802600) qg73h11.x1"
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                                                                                                                                                                                                                                                                                                                             .15772,22543.
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Search completed: January 24, 2002, 02:27:00 Job time: 4473 sec
                                                                                                         Query Match 39.3%; Score 35.4; DB 9; Length 132319; Best Local Similarity 79.2%; Pred. No. 94; Matches 42; Conservative 0; Mismatches 11; Indels 0;
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21910. .22000
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11963. .12120
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13228. .13302
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17337_ .17695
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14556. .14624
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3737. .13885
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16710. .17046
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23259. .23353
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20660. .20941
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8. .15772
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_family="L2"
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	Query Match Length DB	DB	ID	Description
c 1	37.8	42.0	561	13	AQ533830	AQ533830 RPCI-11-
c 2	35.6	39.6	302	10	AV247937	AV247937 AV247937
c 3	34.8	38.7	447	13	B67487	B67487 T25M7TR TAN
c 4		38.7	482	13	AQ968516	A0968516 LERJD03T1
ი 5		38.7	488	13	AQ968397	AQ968397 LERJC21TI
0		38.7	497	13	AQ958266 .	AO958266 LERAW47TH
c 7	34.8	38.7	498	13	B77731	B77731 T28N11TF T
c 8		38.7	623	13	.B30114	B30114 T26F22TFB T
c 9		38.7	627	13	в78178	B78178 T31J11TF TP
10		38.7	640	13	AQ958844	AQ958844 LEREF16T1
c 11	34.8	38.7	643	13	в98363	B98363 T24C11TFB T
c 12	34.8	38.7	660	13	CNSOOWZN	AL094241 Arabidons

FEATURES

Location/Qualifiers

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45	44	43	42	41	40	39	38	37	36	3 5	34	ω G	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13
32.4	32.4	2	,	2	.2	٥.	2	2	2	ν.	۲.	33	33.2	33.2	33.2	33.4	33.6	33.6	33.6	33.6	33.6	33.6	33.6	33.6	33.8	34			4	34.8	4	
36.0	36.0	36.2	36.2	36.4	36.4	36.4	36.4	36.4	36.4	36.4	36.4	36.7	36.9	36.9	36.9	37.1	37.3	37.3	37.3	37.3	37.3	37.3	37.3	37.3	37.6	37.8	38.0	38.2	38.2	38.7	38.7	38.7
589	366	553	510	958	949	944	899	843	589	473	420	1101.	652	526	463	432	913	676	552	413	376	306	240	240	867	871	923	638	607	798	743	683
13	13	13	13	13	13	13	13	13	13	13	11	13	11	11	11	10	13	13	13	13	10	11	10	10	13	13	13	13	13	13	13	13
AZ247746	BH014409	AQ698845	AZ384026	AZ687864	CNS018DG	AZ543633	вн136018	AZ549410	AQ026620	AQ001587	Z38090	CNS00K0G	BG603423	BG603424	BG603509	AA149033	вн132369	AQ635998	AZ065684	AQ798320	AV760889	C24362	AU072714	AU072517	CNS00CX5		вн132631			AQ956484		AQ968517
	BH014409 TDGBL42TH	AQ698845 HS_5557_B	AZ384026 1M0141G19	AZ687864 ENTHB28TF	AL109198 Drosophil	AZ543633 ENTDL72TF	BH136018 ENTOL96TF	AZ549410 ENTFG80TF	AQ026620 CIT-HSP-2	AQ001587 CIT-HSP-2	Z38090 ATTS4230 Ve	AL076967 Drosophil	BG603423 EST502513	BG603424 EST502514	BG603509 EST502599	AA149033 zo03h12.s	BH132369 ENTNH76TR	AQ635998 RPCI-11-4	AZ065684 RPCI-23-4	AQ798320 HS_3160_A	AV760889 AV760889	C24362 C24362 Dict	AU072714 AU072714		AL060052 Drosophil	AZ680048 ENTKK43TR	BH132631 ENTOP70TR	AZ523727 222PbH02				

ALIGNMENTS

		JOURNAL COMMENT	AUTHORS TITLE	ORGANISM	ACCESSION VERSION KEYWORDS SOURCE	LOCUS DEFINITION
Library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html. Seg primer: T7 Class: BAC ends.	Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850 Tel: 301 838 0200 Fax: 301 838 0208 Email: hbeetigr.org Clones are derived from the human BAC library RPCI-11. For BAC	Map Building Unpublished (1997) Other_GSSs: RPCI-11-379L24.TJ Contact: Shaying Zhao, William Nierman, Mark Adams	Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter , J.C. Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready	Homo Sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 561)	, DNA sequence. AQ533830 AQ533830.1 GI:4845520 GSS. human.	AQ533830 561 bp DNA GSS 18-MAY-1999 RPCI-11-379L24.TV RPCI-11 Homo sapiens genomic clone RPCI-11-379L24

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ACCESSION
VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTS (Konno, H., et al. 1999)
Unpublished (1999)
Contact: Yoshihide Hayashizaki
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,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
                                                                                                                                                                          Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
                                                                                                                                                                                                                                                                                                                                                                                        Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
88 c 72 g 192 t
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/db_xref="GDB:7645439"
/db_xref="taxon:9606"
/clone="RPCI-11-379L24"
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/sex="Male"
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Hayashizaki
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53; Conserv
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T25M7TR TAMU
                               Contact: Steve Rounsley
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Rounsley, S.D., Field, C.E.,
                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids_II; Brassicales; Brassicaceae; Arabidopsis.
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          Department of Eukaryotic Genomics
                                                                              A BAC End Sequence Database for Identifying Minimal Overlaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                             Berry, K., Granger, D.,
Institute for Genomic
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58 c 62 g 96 t
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Project of Genome Exploration Research Group in Rike
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/dev_stage="0 day neonate"
/lab_host="DH10B"
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/strain="C57BL/6J"
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/clone="4833401E05"
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Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based
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Class: BAC ends
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The Institute for Genomic Research
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Arabidopsis thaliana
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                                                                                                                                                                                    For addtional information, see http://www.tigr.org/tdb/at/at.html
Similar to A. thaliana chloroplast sequence (GB:AP000423)
                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
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                                                                                                                                                                                                                   Email: at@tigr.org
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/clone_lib="LERG"
/note="Organ: Leaf; Vector: pUC19JK; Total genomic sheared to 0.4-0.7 Kbp before ligation."
                                                   /strain="Landsberg er
/db_xref="taxon:3702"
/clone="LERJD03"
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/note="Vector: BeloBACII;
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/clone="T25M7"
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/strain="Columbia"
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Contact: Xiaoying Lin
The Institute for Genomic Research
The Institute for Genomic Rockville,
                                                                                                                                                                                                                                                                                                                        Class: shotgun
                                                                                                                                                                                                                                                                                                                                   For addtional information, see http://www.tigr.org/tdb/at/at.html
Similar to A. thaliana chloroplast sequence (GB:AP000423)
Seq primer: TR
                                                                                                                                                                                                                                                                                                                                                                                          9712 Medical Center
Tel: 301 838 0200
Fax: 301 838 0208
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Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based
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/note="Organ: Leaf; Vector: pUC19JK; Total genomic DNA was sheared to 0.4-0.7 Kbp before ligation."
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/strain="Landsberg erecta"
/db_xref="taxon:3702"
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Unpublished (2000)
Contact: Xiaoying Lin
The Institute for Genomic Research
The Institute for Genomic Rockville,
                               1 (bases 1 to 498)
Rounsley,S.D., Field,C.E., Bass,S., Linher,K., Linher,K., Golder, Berry,K., Granger,D., Suh,E., Wible,C., Adams,M.D. and Venter
                                                                                    Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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Buell, C.R., Lin, X., Pal, G., Barnstead, M., Bowman, C., Utterbach, T.
Feldblyum, T., Liang, F., Creasy, T. and Fraser, C.M.
Genomic survey sequencing of Landsberg erecta ecotype of
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Spermatophyta; Magnolyophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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For addtional information, see http://www.tigr.org/tdb/at/at.html
Similar to A. thaliana chloroplast sequence (GB:AP000423)
Seq primer: TR
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/db_xref="taxon:3702"
/db_cref="taxon:3702"
/db_ne="LERAW47"
/clone="lib="LERA"
/note="Organ: Leaf; Vector: pHOS1; Total genomic DNA was sheared to 0.9-1 Kbp before ligation."
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Best Local
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TZ6F22TFB TAMU Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis Genomic Sequencing Unpublished (1997) Other_GSSs: TZ6FZ2TRB
                                                                                                                                                                                                                                                             Contact: Steve Rounsley
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
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                           High quality sequence stop: 623
Location/Qualifiers
                                                                                                                            Email: rounsley@tigr.org
Seq primer: M13-21
                                                                                                                                                                                              Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         \begin{array}{ll} \textbf{Venter, J.C.} \\ \textbf{Use of a BAC End Sequence Database To Identify Minimal Overlaps for} \\ \end{array} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; Streptophyta; Tracheophyta; Spermatophyta;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana
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Location/Qualifiers
                                                                                             Class: BAC ends
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Seq primer: M13-21
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The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Steve Rounsley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thale cress.
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/strain="Columbia"
/db_xref="taxon:3702"
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Pred. No. 9.9e+02;
0; Mismatches 27
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Best Local S
Matches 51
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 ch 38.7%;
l similarity 65.4%;
51; Conservative
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B78178
                                                                                                                                                                                                                                                            Seq primer: M13-21
Class: BAC ends
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Rounsley,S.D., Field,C.E., Bass,S., Linher,K., Linher,K., Golder, Berry,K., Granger,D., Suh,E., Wible,C., Adams,M.D. and Venter
                                                                                                                                                                                                                                                                                                                                                                            Contact: Steve Rounsley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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                                                                                                                                                                                                                                                                                                                                  9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                             Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                         Email: rounsley@tigr.org
                                                                                                                                                                                                                                                                                                                                                 The Institute for Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosidae; eurosids II; Brassicales; Brassicaceae;
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301 838 0208
                                                                                                                                                                                                                                quality sequence stop: 627
Location/Qualifiers
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                                                                                  /sex="hermaphrodite"
/note="Vector: BeloBACII; Site_1:
; Produced by Rod Wing"
87 c 99 g 176 t
                                                                                                                                                           /db_xref="taxon:3702"
/clone="T31J11"
                                                                                                                                                                                       /strain="Columbia"
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/clone="T26F22"
                                                                                                                                                                                                   organism="Arabidopsis thaliana"
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Score 34.8; D
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 DB 13;
3.9e+02;
nes 27;
                                                                                                                                                                                                                                                                                                                                  MD 20850, USA
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T31J11, DNA
                             627;
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Best Local
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AQ958844
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Contact: Xiaoying Lin
The Institute for Genomic Research
The Institute for Genomic Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Class: shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: at@tigr.org
For addtional information, see http://www.tigr.org/tdb/at/at.html
Similar to A. thaliana chloroplast sequence (GB:AP000423)
Seq primer: TR
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Tel: 301 838 0200
Fax: 301 838 0208
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sheared to 0.6-0.8 Kbp before ligation."
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/strain="Landsberg erecta"
/db_xref="taxon:3702"
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Submitted (25-JUN-1999) Genoscope -
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Arabidopsis thaliana genome survey sequence T7 end of BAC T1202 of TAMU library from strain Columbia of Arabidopsis thaliana, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: rounsley@tigr.org
Seq primer: M13-21
Class: BAC ends
                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosida II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 660)
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Tel: 301 838 0200
Fax: 301 838 0208
                          Direct Submission
                                       Genoscope.
                                                                           Unpublished
                                                                                              Samson, D., Saurin, W.,
                                                                                                               Salanoubat, M.,
                                                                                                                                                                                                            Arabidopsis thaliana
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AL094241.1 GI:5295395
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Department of Eukaryotic Genomics
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Unpublished (1997)
Other_GSSs: T24C11TF T24C11TRB
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Rounsley,S.D., Field,C.E., Bass,S., Linher,K., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Adams,M.D. and Venter
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/strain="Columbia"
/db_xref="taxon:3702"
/clone="T24C11"
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/note="Vector: BeloBACII; Site_1: HindIII;
/ Produced by Rod Wing"
90 c 103 g 181 t 1 others
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                  Email: atetigr.org
For addtional information, see http://www.tigr.org/tdb/at/at.html
Similar to A. thaliana chloroplast sequence (GB:APO00423)
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/clone="T1202"
                                                                                               /clone_lib="LERG"
/note="Organ: Leaf; Vector: pUC19JK; Total genomic sheared to 0.4-0.7 Kbp before ligation."
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Contact: Xiaoying Lin
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: at@tigr.org
For addtional information, see http://www.tigr.org/tdb/at/at.html
Similar to A. thaliana chloroplast sequence (GB:AP000423)
Seq primer: TF
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/strain="Landsberg erecta"
/db_xref="taxon:3702"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaeae; Arabidopsis.

1 (bases 1 to 798)

Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utterbach, T.,
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Similar to A. thaliana chloroplast sequence (GB:AP000423)
Seq primer: TR
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Tel: 301 838 0200
Fax: 301 838 0208
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The Institute for Genomic Research
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/note="Organ: Leaf; Vector: pHOS1; Total genomic DNA was
sheared to 0.9-1 Kbp before ligation."
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Copyright (c) 1993 - 2000
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US-08-378-313-18
US-08-378-313-18
US-08-086-410-23
US-08-086-410-23
US-08-086-410-23
US-08-764-100-8
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10-1/C 1, Application 1, Application 1, S522133 INFORMATION: OF INVENTION: OF INVENTION: OF SEQUENCES: PONDENCE ADDRE ESSEE: Darby ET: 805 Third 10022-7513 INTERNATION: OF SEQUENCES: PONDENCE ADDRE ESSEE: Darby ET: 805 Third INCOUNTYPE: FLOP UTER: 1BM PC UTER: 1BM PC ATING SYSTEM: WARE: PAtentI T APPLICATION ICATION UNMEER RENCE/DOCKET NUMEER RENCE/DOCKET NUMEER RENCE/DOCKET NUMEER RENCE/DOCKET NUMEER 1993 STRATION NUMBER 1993 STRATION NUMBER 10090715; Ad STRATION NUMBER 10090715; Ad ETICAL: NO MMUNICATION IN MMUNICATION IN MMUNICATION IN MMUNICATION IN MMUNICATION NUMBER 10090715; Ad STRATION NUMBER 10090715; AD ETICAL: NO ENCE: NO ENCE: NO ENCE: NO ENCE: NISM: PLASMOD AL SOURCE: BI PVMB3.3.1	23333333333333333333333333333333333333
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Query Match

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Score 31.2;

DB 1;

Length 3337;

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RESULT 2
US-08-719-822B-1/c
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                                                                                                                                                                     Query Match
Best Local Similarity
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COMPUTER REALDABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
TYCTEM: PC-DOS/MS-DOS
TYCTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Gogoris, Adda
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 59
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                           HYPOTHETICAL:
ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 3337 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                            138
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TELEFAX: 236687
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                                 ATTAAAAGAAAAGCAA 63
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(212)753-6237
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; Sequence 79, Application, patent No. 6090620; GENERAL INFORMATION: APPLICANT: Fu, Ying APPLICANT: Yu, Charan APPLICANT: Oshima,
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                                                                                            US-08-781-891-79
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                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
CLONE: PVMB3.3.1
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 59
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)527-7700
TELEFAX: (212)753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/7: FILING DATE: 09/30/96 ATTORNEY/AGENT INFORMATION: NAME: Gogoris, Adda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELLEFAX: 12. TELLEFAX: 236687
                                                                                                                                                                                                                 138 AATATATATGTATATATAGCAGTTTTTATAGATTATTTTTATCTTACTGTTGAAGCATGA 79
                                                                                                                                                       78
                                                                                                                                                                     70 agtccaatgaaagcaa 85
                                                                                                                                                                                                                               10 attatttcaaagtttactgtaatttttatgttttcatgttttcttattgtttggagcaata 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 29,714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 10022-7513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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                                             379, Apr
No. 6090620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
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                                                                           Application US/08781891
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 Yu, Chang-En
Oshima, Junko
                               Fu, Ying-Hui
                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           double
                                                                                                                                                                                                                                                                                           34.7%;
63.2%;
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Pred. No. 5.3;
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TITLE OF INVENTION: GETITLE OF INVENTION: WE NUMBER OF SEQUENCES: 2

Schellenberg, Gerald D.
VENTION: GENE AND GENE PRODUCTS RELATED TO
ENTION: WERNER'S SYNDROME

ADDRESSEE:

SEED and BERRY LLP

APPLICANT:

Mulligan, John

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; TYPE: DNA; ORGANISM: Solanum tuberosum US-08-894-731-2
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                                                                                                                            SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                            GENERAL
                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08894731 Patent No. 6084089
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Query Match
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,891
FILING DATE: 27-DEC-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
                                                                                                                                       CURRENT APPLICATION NUMBER: US/08/894,731
CURRENT FILING DATE: 1997-10-27
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                               APPLICANT: MINE, TOShiki
APPLICANT: CHYAMA, Akio
APPLICANT: HIYOSHI, TOTU
APPLICANT: KASAOKA, Keisuke
TITLE OF INVENTION: COLD-INDUCIBLE PROMOTER SEQUENCE
FILE REFERENCE: 760-234P
                                                                                                                                                                                                                                                                                                                                                                                                                                                   76895 GGATATACTTCCATT 76911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76835 ATGCAATAGGGTATTTTGÀAGGTTTTCTGTATGTTTTTCTGTAGAAAAGTTATCTCÀAAGGG 76894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (206) 682-6031
NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                         LENGTH: 4140
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ggagcaataagtccaat 77
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                                                                                                                                                                                                                                                                                                                           INFORMATION:
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 33.38;
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Pred. No. 9;
 Score 30;
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 DB 3;
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Length 4140;
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US-08-378-313-18
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                                                                                                        Matches
                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/862,493
FILING DATE: 02-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: THEOLOGIS, ATH APPLICANT: SATO, TAKAHIDO
1552 GGGTCAAT 1559
                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 29
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 856-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: CONTROL OF FRUIT RIPENING THROUGH TITLE OF INVENTION: GENETIC CONTROL OF ACC SYNTHASE SUNTHESIS
                                                                                                                                                                                                                                                                                               TELEFAX: 1.06141
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                      61 ggagcaat 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Palo Alto
STATE: California
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                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                            NAME: MURASHIGE, KATE REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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                                                                                                                                                                                                                                                    nucleic acid
                                                                                                                                                                                                                                                                     1703 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       755 Page Mill Road
                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                         (415) 494-0792
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                                                                                                                    32.98;
64.78;
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                                                                                                                    Score 29.6;
Pred. No. 12;
                                                                                                      Mismatches
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                                                                                                                                DB 4;
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US-08-062-632-4/c

Sequence

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Application US/08062632

Patent No. 5712090

GENERAL INFORMATION:

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                                                                                                                                         Patent No. 530202
Patent No. 530202
Patent No. 530202
Patent No. 530202
Patent No. 530202
Patent No. 530202
                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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ATTORNEY/AGENT INFORMATION:
NAME: Brady Jr., James W.
REGISTRATION NUMBER: 32,115
REFERENCE/DOCKET NUMBER: 1897
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)/85-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (202)887-0689
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 2334 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                             APPLICANT: APPLICANT:
                                                           APPLICANT:
APPLICANT:
                                                                                          APPLICANT:
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APPLICANT: Stipkovits, Lasio
APPLICANT: Minion, F. Chris
TITLE OF INVENTION: PCR-Base
TITLE OF INVENTION: Hyopneumo
APPLICANT
                APPLICANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                   176 TCTGC 172
                                                                                                                                                                                                                                                                                                                             236 ATTAAGAAAATCGCTTAATTATTGGTGTTATTTTTATTTTTACTTGTGTTTTAATAGTT 177
                                                                                                                                                                                                                                                                                              61 ggagc 65
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FILING DATE: 18-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity es 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                       Application US/07920519
                                                       FERRARA, PASCUAL
GUILLEMOT, JEAN-CLAUDE
KAGHAD, MOURAD
LEGOUX, RICHARD
LOISON, GERARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Dickstein,
2101 L. St. N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
SALOME, MARK
                           LARBRE, ELIZABETH LUPKER, JOHANNES
                EPLATOIS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA (genomic)
                                                                                                                                         DANIEL
                                                                                                                                                                                                                                                                                                                                                                                                     31.3%;
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              PASCUAL
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                                                                                                                                                                                                                                                                                                                                                                                        ; Score 28.2; Di
; Pred. No. 28;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2334;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                      Sequence 23, Application US/08086410 Patent No. 5407822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                              APPLICANT: LEPLATOIS, Pascal
APPLICANT: LOISON, Gerard
APPLICANT: PESSEGUE, Bernard
APPLICANT: SHIRE, David
TITLE OF INVENTION: Artificial profile of INVENTION: of proteins in
                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL: NO
IMMEDIATE SOURCE:
GTONE: Fragment D
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SEQUENCE CHARACTERISTICS:
LENGTH: 1013 base pairs
                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                   NUMBER OF SEQUENCES:
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TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                       944 AACAAGTGAATGAATG 929
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CITY: A
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 STREET:
                                 ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/07/920,519
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King Street Station, Suite 500, 1800 Diagonal Road, PO Box 299
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                                 FOLEY & LARDNER
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Pred. No.
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

COUNTRY:

ALEXANDRIA

VIRGINIA USA

22313-0299

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                                                                                                                                                                                                                                                                               Sequence
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Best Local Similarity
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LENGTH: 1013 base pairs
                                                                                                                                                              APPLICANT:
APPLICANT:
                                                                                                   APPLICANT:
                                            TITLE OF INVENTION: TITLE OF INVENTION:
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MOLECULE TYPE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
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APPLICATION NUMBER: US 07/768,01
FILING DATE: 02-0CT-1991
APPLICATION NUMBER: FR 89 17467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                             NUMBER OF SEQUENCES:
                                                                                                                                                   APPLICANT
                                                                                                                                                                                            APPLICANT:
                                                                                     APPLICANT:
                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (703) 683-4109
TELEX: 899149
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REGISTRATION NUMBER: 28,665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/086,410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic
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55410
                                                                                                                                                                                                                                                    INFORMATION:
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                                                                                                                                                                                                                                                                               Application US/08314586
                                                                                    LAURENT, PATRICK
                                                                                                  LEPLATOIS, PASCUAL SALOME, MARK
                                                                                                                                  LUPKER,
                                                                                                                                                                                         GUILLEMOT, JEAN
KAGHAD, MOURAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Foley & Lardner
             ADDRESS
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JOHANNES
                                                       URATE OXIDASE ACTIVITY PROTEIN, RECOMBINANT GENE CODING THEREFO
                                                                                                                                                               GERARD
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60.5%;
                                          RECOMBINANT GEN
MICROORGANISMS
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Pred. No. 30;
0; Mismatches
                                            AND
                                            TRANSFORMED CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 1013;
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                                                          THEREFOR, EXPRESSION VECTOR,
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US-07-667-276A-1
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Best Local S
Matches 46
                                                                                                                                                                                                                                                     Sequence 1, Application Patent No. 5470971 GENERAL INFORMATION:
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IMMEDIATE SOURCE:
CLONE: Fragment D
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TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                     NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Welser & Associates
STREET: 230 S. Fifteenth Street,
                                                                                                                                                                      APPLICANT: Kondo, Keiji
APPLICANT: Inouye, Masayori
TITLE OF INVENTION: STRESS-INDUCED PROTEINS, GENES CODING
TITLE OF INVENTION: THEREFOR, TRANSFORMED CELLS OF ORGANISMS, METHODS AND
TITLE OF INVENTION: APPLICATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
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CITY: Washington
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les 46; Conserv
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                        COUNTRY:
                                                                                       CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
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20007-5109
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        Floppy disk
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60.5%;
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30;
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PatentIn Release #1.0, Version #1.25

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OTHER INFORMATION: corresponds to base -474 of;
OTHER INFORMATION: Figure 4 of the application"
US-07-667-276A-1
                                                                                                                                                                                                                                                                                                                                   RESULT 12
US-07-861-458C-4/c
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Best Local 9
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                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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              COMPUTER: IBM PS/2 Model 50Z or 55SX OPERATING SYSTEM: MS-DOS (Version 5.0) SOFTWARE: WordPerfect (Version 5.1) CURRENT APPLICATION DATA:
                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
                                                                                                                                                                                                                      APPLICANT: Marchionni, Mark Andrew APPLICANT: Johnson, Carl D. TITLE OF INVENTION: HOMOLOGY CLONING NUMBER OF SEQUENCES: 142
                                                                                                                                                                                                                                                                                                                                                                                                  1179 GTTCGAAAATT 1189
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LENGTH: 1584 base pairs
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ORIGINAL SOURCE:
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 APPLICATION
                                                                                                             COUNTRY: U.S.A. ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                62 gagcaataagt 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 215-875-8394
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                                                                                                                                              STATE:
                                                                                                                                                                          STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Weiser, Gerard REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
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                                                                                                                                                           Boston
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EDNESS: double
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                                                                                                                                                                        225 Franklin Street
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US/07/861,458C
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Pred. No. 34;
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US-08-463-418-1
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Best Local Similarity
                                                                        ATTORNEY/AGENT TO AME: 7.162

REGISTRATION UMBER: 30,162

REFERENCE/DOCKET NUMBER: 0078

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION 107542-5070
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                                   TELEX: 200154
INFORMATION FOR SEQ ID NO:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                  CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/962,481
FILING DATE: 15-0CT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,418
FILING DATE: 05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 04585/014001
TELECOMMUNICATION INFORMATION:
TELECPHONE: (617) 542-5070
                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                    TELEPHONE: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 02110-2804
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TOPOLOGY: linear
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NVENTION: CRUCIFER ACC SYNTHASE AND USES THEREOF
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Pred. No. 42;
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Best Local Similarity Matches 38; Conserv

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Mismatches

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Gaps

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67.9%;

Pred. No. 46;

; TOPOLOGY: 1: ; MOLECULE TYPE: US-08-463-418-1 STRANDEDNESS: linear double

Matches Best Local Similarity Query Match 40; Conservative 30.4%; Score 27.4; Pred. No. 47; Mismatches DB 2; 21;Length 5613; Indels

0;

Gaps

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B QY 64 g 64 4 aaaaaaattatttcaaagtttactgtaatttttatgttttcatgttttcttattgttgga 63

Qy

В 2093 G 2093

RESULT 14 US-08-764-100-8 Sequence 8, Approximately 5773700 GENERAL INFORMATION: Application US/08764100

APPLICANT: APPLICANT: APPLICANT: Gielen L., Peters, Dirk De Haan, Petrus T. van Grinsven J., Martinus Johannes J. 0

TITLE OF INVENTION: NUMBER OF SEQUENCES: APPLICANT: Goldbach, Robert W Improvements in or Relating to Organic Compounds : 27

CORRESPONDENCE ADDRESS: ADDRESSEE: 975 California Avenue Sandoz Agro, Inc

STREET: 9/J COUNTRY: 94304 USA

CURRENT APPLICATION DATA: COMPUTER READABLE FORM: COMPUTER: IBM PC OPERATING SYSTEM: SOFTWARE: MEDIUM TYPE: PatentIn Release #1.0, IBM PC compatible SYSTEM: PC-DOS/MS-DOS Floppy disk Version #1.25

PRIOR APPLICATION DATA: FILING DATE: 0 APPLICATION NUMBER: 06-DEC-1996 US/08/764,100

APPLICATION NUMBER: FILING DATE: GB 9206016.9 US/08/214,06 US 08/032,235

APPLICATION NUMBER: US 08/032,
FILING DATE: 17-MAR-1993
APPLICATION NUMBER: GB 920601(
FILING DATE: 19-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5773700ris, Allen E
REGISTRATION NUMBER: 34,490 Allen E. 137-1061

TELEPHONE: (415) 354-3592
TELEFAX: (415) 857-1125
NFORMATION FOR SEQ ID NO: 8: REFERENCE/DOCKET NUMBER: 13
TELECOMMUNICATION INFORMATION:

SEQUENCE CHARACTERISTICS: LENGTH: nucleic acid EDNESS: single 602 base pairs

Qy

aaaaaattattcaaagtttactgtaatttttatgttttcatgttttcttattgtt 60

Query Match
Best Local Similarity

30.2%;

Score 27.2; Pred. No. 4

46; DB 1; 18;

Length 642;

Mismatches

Indels

0;

Gaps

0;

Matches

Conservative

Search completed: January 24, 2002, 02:18:58 Job time: 3931 sec

US-08-764-100-8 STRANDEDNESS: FOPOLOGY: linear

Query Match

30.2%; Score 27.2; DB 1; Length 602;

> RESULT 15 US-08-764-100-13/c 밁 Sequence 13, Application US/08764100 Patent No. 5773700 TELEFAX: (415) 857-11 INFORMATION FOR SEQ ID NO: APPLICANT:
> APPLICANT: REFERENCE/DOCKET NUMBER: 13
> TELECOMMUNICATION INFORMATION:
> TELEPHONE: (415) 354-3592 SEQUENCE CHARACTERISTICS: FILING LOTE: US
> FILING DATE: 17-MAR-19
> APPLICATION NUMBER: GH
> APPLICATION NUMBER: GH
> TITING DATE: 19-MARE 1 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA: COMPUTER READABLE FORM:
> MEDIUM TYPE: Floppy disk FILING DATE: 19-MAR(1992)
> ATTORNEY/AGENT INFORMATION:
> NAME: NO. 577370071s, Allen
> REGISTRATION NUMBER: 34,490 CLASSIFICATION: 800 PRIOR APPLICATION DATA: CORRESPONDENCE ADDRESS TITLE OF INVENTION: APPLICANT: NUMBER OF SEQUENCES: LENGTH: 642 base pairs
> TYPE: nucleic acid
> STRANDEDNESS: single FILING DATE: COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS CITY: Palo Alto STATE: CA TOPOLOGY: APPLICATION NUMBER: FILING DATE: APPLICATION NUMBER: ZIP: 94304 COUNTRY: STREET: ADDRESSEE: INFORMATION: 975 California Avenue USA De Haan, Petrus T. Gielen L., Johannes J Goldbach, Peters, Dirk van Grinsven J., Martinus linear Sandoz Agro, O6-DEC-1996) 17-MAR-1993 857-1125 Improvements Compounds US/08/214,064 Robert W US 08/032,235 GB-9206016.9 Allen E. Inc 137-1061 'n Version #1.25 or Relating to Organic

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Result
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Copyright (c) 1993 - 2000 Comp
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/FCTUS_COMB.seq:*
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PCT-US96-0547-43-168
US-08-105-483-168
US-08-105-488-20-1
US-08-105-48-20-1
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US-09-163-162-19
US-09-163-162-19
US-09-163-50-8-4
US-09-166-030-4
US-09-170-916-4
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US-09-235-538-5
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US-08-341-456A-14	US-08-935-312-14 '	US-08-642-274D-104	US-08-629-001A-25	US-08-619-724-3	US-08-771-602D-21	US-08-771-602D-20	US-08-644-116A-6	US-08-905-445-6	US-08-668-128B-6	US-09-490-558-176	US-09-490-558-72	US-08-835-728D-176	US-08-835-728D-72	US-09-249-215-140	US-08-910-408-140	US-08-271-880A-140	US-08-462-437-26
Sequence 14, Appl	Sequence 14, Appl	Sequence 104, App	Sequence 25, Appl	Sequence 3, Appli	Sequence 21, Appl	Sequence 20, Appl	Sequence 6, Appli	Sequence 6, Appli	Sequence 6, Appli	Sequence 176, App	Sequence 72, Appl	Sequence 176, App	Sequence 72, Appl	Sequence 140, App	Sequence 140, App	Sequence 140, App	Sequence 26, Appl

ALIGNMENTS

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us-08-672-215-1
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                                                                                         TELEFAX: (213) 955-044
TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ying Bao, Amy Boggs, Pamela R. Contag,
APPLICANT: Nancy A. Federspiel, Alan Herbert,
APPLICANT: Scott J. Hecker, Francois Malouin
TITLE OF INVENTION: INHIBITORS OF REGULATORY PATHWAYS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ANDRESCED: YILLIAM
                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: FastSEQ for Windows 2.0 CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/672,215
FILING DATE: June 25, 1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                          TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION: NAME: Warburg, Richard J
                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
FILING DATE: Septemb
APPLICATION NUMBER:
FILING DATE:
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STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                      TYPE: nuclei
STRANDEDNESS:
                                                                                                                                                                                                                                  NAME: Warburg, Richard REGISTRATION NUMBER: 3
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                                                                                                                                                                        TELEPHONE:
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                                                                        LENGTH:
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                                                    nucleic acid
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633 West Fifth Street
Suite 4700
                                                                          24 base pairs
                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM Compatible
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                                                                                                                                      GENERAL INFORMATION:
                      APPLICANT: Shiloh, Yosef
TITLE OF INVENTION: MUTATED FORMS OF THE ATAXIA-TELANGIECTASIA GENE AND METHOD
TITLE OF INVENTION: SCREEN FOR A PARTIAL A-T PHENOTYPE
FILE REFERENCE: 22900003
CURRENT APPLICATION NUMBER: US/08/642,274D
CURRENT FILING DATE: 1996-05-03
NUMBER OF SEQ ID NOS: 220
                                                                                                                                                     Sequence 158, Application US/08642274D Patent No. 6200749
   SEQ ID NO 158
                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 13; Conserv
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Best Local Similarity
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NAME: Kohn, Kenneth I.

REGISTRATION NUMBER: 30,955

REFERENCE/DOCKET NUMBER: 220

TELECOMMUNICATION INFORMATION:

TELEPHONE: (810) 539-5050
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SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                               15 AAAAATTATTTC 27
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                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE:
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CLASSIFICATION: 435
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               PatentIn Ver.
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100.08; Pr
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100.0%; Pred. No.
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Pred. No.
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              RESULT
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US-08-105-483-168/c
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TOPOLOGY: linear; MOLECULE TYPE: cDNA PCT-US96-00547-40.
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GENERAL INFORMATION:
APPLICANT: Virogenetics Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 13; Conserv
                                                                 Matches
                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                             TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence:intronic OTHER INFORMATION: sequence
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                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2621
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 13-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US96/00547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: RECOMBINANT POXVIRUS-HTLV, COMPOSITIONS TITLE OF INVENTION: AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
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                               26 ctgtaattttat 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
25 CTGTAATTTTAT 13
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                                                                                                                                                                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: New York
STATE: New Yor
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                                                                                                                                                                                                                                                                                                                                                                   NAME:
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                                                                                                                                                                                                            nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New York
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                                                                 Conservative
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                                                                                                                                                                                                                                                                                               (212) 840-3333
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                                                                               14.4%;
100.0%;
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                                                                               Score 13; pred. No.
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; Pred. No.
                                                                 Mismatches
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6.8e+02
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                                                                                               Length 38
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Sequence 168, Application US/08105483 Patent No. 5494807

GENERAL INFORMATION:

No.

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US-08-709-209-168/c
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                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                       Sequence 168, Application US/08709209 Patent No. 5762938
                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local Similarity
                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (212) 840-0712 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                          APPLICANT: Paoletti, TITLE OF INVENTION: (TITLE OF INVENTION: (TITLE OF INVENTION)
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
OPERATING SYSTEM: PC-DOS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/105,483
FILING DATE: 12-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 550
STREET: New York
CITY: New York
TWATE: NY
                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 840-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 06-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 06-MAR-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                            STREET: 530 Fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2400
                                                               COUNTRY: U
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                                                                                                                                          ADDRESSEE: C/O William S. Frommer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Curtis, Morris & Safford ADDRESSEE: c/o William S. Frommer STREET: 530 Fifth Avenue
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                                                                                                                             530 Fifth Avenue
                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Paoletti,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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100.0%; Pro
compatible
PC-DOS/MS-DOS
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                                                                                                                                                                                                                         GENETICALLY ENGINEERED VACCINE
                                                                                                                                                                                            462
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US-08-303-275-56/c
; Sequence 56, Application US/08303275
; Patent No. 5766598
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Matches 13; Conserv
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                                                                                           FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/897,382
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: FIORMEY, William S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (212) 840-07 INFORMATION FOR SEQ ID NO:
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2420
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION DATA:
PRIOR APPLICATION NIMBER: US 08/105,483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Paoletti, Enzo
APPLICANT: Tartaglia, James
APPLICANT: Cox, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
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APPLICATION NUMBER: US 0
FILING DATE: 06-MAR-1992
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 840-3333
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                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U
ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                               CITY: New York
STATE: New York
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FILING DATE: 12-AUG-1993
                                                                                                                                                                                                                             APPLICATION NUMBER:
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STRANDEDNESS: singl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2400
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                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: C/O William S. Frommer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Frommer, William S. REGISTRATION NUMBER: 25,5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/709, 209
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; Pred. No.
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INFORMATION FOR SEQ ID NO:

56:

SEQUENCE CHARACTERISTICS

LENGTH:

39 base pairs

TYPE: nucleic acid
STRANDEDNESS: single

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US-08-458-101-168
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Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                            TELEFAX: (212) 840-071:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,101
FILING DATE: 01-JUN-1995
CLASSIFICATION: 424
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: COX, William I.

APPLICANT: Audonnet, Jean-Christophe Francis
APPLICANT: Audonnet, Jean-Christophe Francis
APPLICANT: Gettig, Russell Robert
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
TITLE OF INVENTION: STRAIN
NIMBER OF SEQUENCES: 467
                                                                                                                                               NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE,DOCKET NUMBER: 456
TELECOMMUNICATION INFORMATION:
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NAME: Frommer, William C
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STATE: NY
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                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Curtis, Morris & Safford ADDRESSEE: c/o William S. Frommer STREET: 530 Fifth Avenue
                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10036
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                                                                  LENGTH:
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                               nucleic acid
pucleic acid
pedness: single
                                                                                                                   E: (212) 840-3333
(212) 840-0712
                                                                                                                                                                                                                                                                                                                                                                                                         USA
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Taylor, Jill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pincus, Steven E.
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Johnson, Gerard P.
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             linear
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                                                                                                     168:
                                                                                                                                                                      454310-2740
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6.7e+02;
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Query Match

14.48;

Score 13;

DB 1;

Length 39;

RESULT

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US-08-271-880A-201
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                                                                Best Local Similarity Matches 12; Conserv
                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/271,880
FILING DATE: July 7, 1994
PRIOR APPLICATION DATA: including a PRIOR APPLICATION DATA: described I PRIOR APPLICATION NUMBER: 08/103,243
FILING DATE: August 6, 1993
APPLICATION NUMBER: 07/882,886
FILING DATE: May 14, 1992
ATTORNEY/AGENT INFORMATION:
NAME: DATE: DATE: AUGUST 6, 1993
APPLICATION NUMBER: 07/882,886
FILING DATE: May 14, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: IBM P.C. DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: METHOD AND REAGENT FOR INHIBITING TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS TITLE OF INVENTION: REPLICATION NUMBER OF SEQUENCES: 232
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STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
                               74 caatgaaagcaa 85
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                                                                                                                                                                                                                                                                                   TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                     NAME: Warburg, Richard REGISTRATION NUMBER: 3
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25 CTGTAATTTTTAT 13
2 CAATGAAAGCAA 13
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: California
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67-3510
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                                                                 Conservative
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                                                                                 Score 12; DB 1; 1; Pred. No. 2.2e+03
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0; Mismatches 0;
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                                                           Sequence 201, Application US/09249215
Patent No. 6159692
GENERAL INFORMATION:
APPLICANT: Kenneth G. Draper
                                                                                                                                                                                                                                               Best Local Similarity 100. Matches 12; Conservative
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                                                                                                                                                                                                                                                                                Query Match
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INFORMATION FOR SEQ ID NO:
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APPLICANT:
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MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: James D. Thompson
TITLE OF INVENTION: METHOD AND REAGENT FOR INHIBITING
TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS
TITLE OF INVENTION: REPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: August 6, 1993
APPLICATION NUMBER: 07/882,886
FILING DATE: May 14, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 20 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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SOFTWARE: FastSE
                                                                                                                                                                                                    74 caatgaaagcaa 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/271,880 FILING DATE: July 7, 1994 APPLICATION NUMBER: 08/103,243 FILING DATE: August 6, 1993
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                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                          ENGTH:
                                                                                                                                                                                       CAATGAAAGCAA 13
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633 West Fifth Street
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Dan T. Stinchcomb
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             James McSwiggen
Dan T. Stinchcomb
                                            Bharat Chowrira
James D.
                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                 13.3%;
100.0%;
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Pred. No.
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                                                     CURRENT APPLICATION NUMBER: US/09/163,162
CURRENT FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 19
                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                     Sequence 19, Application US/09163162 Patent No. 6077709
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                        APPLICANT: Bennett, C. Frank
APPLICANT: Ackermann, Elizabeth J.
APPLICANT: Swayze, Eric E.
APPLICANT: Cowsert, Lex M.
TITLE OF INVENTION: ANTISENSE MODULATION OF
FILE REFERENCE: RTS-0008
ORGANISM: Artificial Sequence
                     LENGTH: 18
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 201:
SEQUENCE CHARACTERISTICS:
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mes 12; Conserv
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OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,215
FILING DATE: 12-Feb-1999
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
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APPLICATION NUMBER: 08/910,408
FILING DATE: <Unknown>
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: METHOD AND REAGENT FOR INHIBITING HUMAN IMMUNODEFICIENCY VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 14 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/103,243
FILING DATE: August 6, 1993
APPLICATION NUMBER: 07/882,886
FILING DATE: May 14, 1992
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REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 20
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Suite 4700
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nilarity 100.0%;
Conservative 0
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                                                                                                                                                                Survivin EXPRESSION
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FEATURE:

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; OTHER INFORMATION: Antisense Oligonucleotide
US-09-286-407-19
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US-09-286-407-19
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: Sequence 6, Application US/08661507

: Patent No. 5814490
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Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 12; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%;
Matches 12; Conservative (
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APPLICANT: Ackermann, Elizabeth J.
APPLICANT: Swayze, Eric E.
APPLICANT: Cowsert, Lex M.
TITLE OF INVENTION. ANTISENSE MODULATION OF SURVIVIN EXPRESSION
FILE REFERENCE: ISPH-0349
FILE REFERENCE: ISPH-0349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/286,407A CURRENT FILING DATE: 1999-04-05 NUMBER OF SEQ ID NOS: 48
                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 18
                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/661,507
                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fugit, Donna R.
                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Spears, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Franklin Lakes
STATE: NJ
COUNTRY: US
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                                                           FILING DATE:
                                                                                                                                                                                                                 ZIP: 07417
                                                                                                                                                                                                                                                                                          ADDRESSEE: R. J. Rodrick, Becton Dickinson and Company STREET: 1 Becton Drive
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Pred. No.
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2.1e+03;
hes 0;
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; TOPOLOGY: linear US-08-855-085-4
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US-08-855-085-4/c
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                                                       Best Local Similarity Matches 12; Conserv
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                                                                                Query Match
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                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Fugit, Donna R.
REGISTRATION NUMBER: 32,1:
REFERENCE/DOCKET NUMBER: 1
INFORMATION FOR SEQ ID NO: 4:
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REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO:
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APPLICANT:
APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DM PC COMPATION
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1:30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Walker, George T TITLE OF INVENTION: Detection TITLE OF INVENTION: Fluores
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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1 GTTTTCATGTTT
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                           39 gttttcatgttt 50
                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                   TYPE: nucleic acid
                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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milarity 100.0%;
Conservative 0
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1 Becton Drive
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Pitner, James B.
Schram, James L.
                                                      13.3%;
ilarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Linn,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carl P
                                                                                                                                                                                                                                                                                       435
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                                                                      Score 12;
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Pred. No.
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                                                       Mismatches
                                                                    DB 2; Lo
2.1e+03;
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US-08-865-675-4/c
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                                                                                                                                                                                                                                                          Sequence 4, Application US/08865675 Patent No. 5928869
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Best Local Similarity
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                                                                                                                                APPLICANT: Nadeau, James G.
APPLICANT: Pitner, James B.
APPLICANT: Linn, Carl P.
APPLICANT: Schram, James L.
TITLE OF INVENTION: DETECTION
TITLE OF INVENTION: FLUORESCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Nadeau, James G.
APPLICANT: Pitner, James B.
APPLICANT: Schram, James L.
APPLICANT: Linn, Carl P.
APPLICANT: Vonk, Glenn P.
APPLICANT: Walker, George T.
TITLE OF INVENTION: Detection
TITLE OF INVENTION: Fluoresceu
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INFORMATION FOR SEQ ID NO: 4:
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NAME: Fugit, Donna R.
REGISTRATION NUMBER: 32,135
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PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
COUNTRY: US
ZIP: 07417
                                  CITY: Franklin Lakes
STATE: NJ
                                                         ADDRESSEE: R. J. NOULE.
STREET: 1 Becton Drive
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                                                                                 J. Rodrick, Becton Dickinson and Company
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                                                                                                                                     PLUORESCENCE QUENCHING
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100.0%; Pred. No
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US-08-933-749-5/c
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Best Local 9
                                                                                     REFERENCE/DOCKET NUMBER: INFORMATION FOR SEQ ID NO: 5:
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                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Fugit, Donna R.
REGISTRATION NUMBER: 32,135
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LENGTH: 21 base pairs
TYPE: nucleic acid
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: R. J. Rodrick, Becton Dickinson and Company
STREET: 1 Becton Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Linn, Carl P.
TITLE OF INVENTION: Detection of Nucleic Acids
TITLE OF INVENTION: Fluorescence Quenching
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Fugit, Donna R.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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ZIP: 07417
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CLASSIFICATION:
                  STRANDEDNESS:
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                                                  ENGTH:
                           nucleic acid
                                                  21 base pairs
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Linn, Carl P.
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linear
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              single
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100.0%; Pred. No.
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; TOPOLOGY: linear US-09-237-510-4
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Best Local Similarity
Matches 12; Conserv
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                                       APPLICANT: Schram, James L.
APPLICANT: Linn, Carl P.
APPLICANT: Vonk, Glenn P.
APPLICANT: Walker, George T.
TITLE OF INVENTION: Detection
TITLE OF INVENTION: Fluoresce
                                                                                                                                                                              GENERAL INFORMATION:
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            CORRESPONDENCE ADDRESS:
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LENGTH: 21 base pairs
TYPE: nucleic acid
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NAME: Fugit, Donna R.
REGISTRATION NUMBER: 32,135
REFERENCE/DOCKET NUMBER: P-
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APPLICANT: SChram, James L.
TITLE OF INVENTION: BETECTI
TITLE OF INVENTION: FLUORES
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                                                                                                                                                                                                                                                                                                                                      39 gttttcatgttt 50
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION:
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1 Becton Drive
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Pitner, James B:
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Pitner, James B.
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                                          Fluorescence
                                                          Detection of
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); Mismatches 0;
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                                                            Nucleic Acids
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. 2.1e+03
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Best Local Similarity
Matches 12; Conserv
FILING DATE:
FILING DATE:
FILING DATE:
ASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Highet, David W.
REGISTRATION NUMBER: 30,265
REFERENCE/DOCKET NUMBER: p-40:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 847-5317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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REGISTRATION NUMBER: 32
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO:
                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/964,020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Vonk, Glenn P.
APPLICANT: Little, Michael C.
TITLE OF INVENTION: Att and M
TITLE OF INVENTION: Detection
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STREET: 1 Becton Driv
CITY: Franklin Lakes
                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/120,916
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                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Richard J. Rodrick - Becton, Dickinson and
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1 Becton Drive
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1 Becton Drive
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Pred No.
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2.1e+03
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Length 21;

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Gaps

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RESULT 23
US-09-599-164-5/c
: Sequence 5, Application US/09599164
: Patent No. 6261784
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Best Local Similarity 100
Matches 12; Conservative
                                                                                                                                                           Matches
                                                                                                                                                                                           Query Match
                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: FUGIT, Donna R.
REGISTRATION NUMBER: 32,135
REFERENCE/DOCKET NUMBER: P-
INFORMATION FOR SEQ ID NO: 5:
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INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Detection of Nucleic Acids by TITLE OF INVENTION: Fluorescence Quenching NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Pitner, James B. APPLICANT: Linn, Carl P.
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Franklin Lakes
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                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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Hsieh, Helen V.
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100.0%; Pred. No.
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2.1e+03;
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US-08-727-003A-10/c
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                                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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TITLE OF INVENTION:
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APPLICANT: Pitner, James B.
APPLICANT: Lin, Carl P.
TITLE OF INVENTION: Detection of Nucleic Acids by
TITLE OF INVENTION: Fluorescence Quenching
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Fugit, Donna R.
REGISTRATION NUMBER: 32,
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OPERATING SYSTEM: PC-DOS/MS DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
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                                                                                                                                                             NUMBER OF SEQUENCES:
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                                                                            CITY: Palo Alto
STATE: California
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                                                               COUNTRY:
                                                                                                            STREET:
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                                                  94306-1840
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                                                             United States of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                    Gruenert,
                                                                                                                           PETERS, VERNY, JONES
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                 Diskette -
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100.0%;
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A METHOD AND ASSAY FOR
DETECTIONOF THE EXPRESSION
OF ALLELE-SPECIFIC MUTATIONS
BY ALLELE-SPECIFIC IN SITU
                                                                                                                                                                        POLYMERASE CHAIN REACTION
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                3.5 inch,
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Pred. No.
                                                               America
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                1.44 Kb storage
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: FILING DATE: Octobe CLASSIFICATION: 435

October 8, 1996

US/08/727,003A

OPERATING SYSTEM: SOFTWARE: Wordper

Wordperfect 5.1

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RESULT 26
US-08-210-762E-31
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                                                                                                                                 Query Match
Best Local Similarity
Matches 12; Conserv
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LENGTH: 23
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CURRENT FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 07/933,471
EARLIER FILING DATE: 1992-08-21
                                                                                                                                                                                                                                                                                                                                                                                      EARLIER APPLICATION NUMBER: 08/409,544 EARLIER FILING DATE: 1995-03-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gruenert, Deiter C.
APPLICANT: Kunzelmann, Karl
TITLE OF INVENTION: GENE THERAPY BY SMALL FRAGMENTS HOMOLOGOUS REPLACEMENT
FILE REFERENCE: 480.18-1(HV)
                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 87
                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (415)324-1
TELEFAX: (415)324-167
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                      TYPE: DNA
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LENGTH: 23 base pairs
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/0 FILING DATE: October 10, ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                               59 ttggagcaataa 70
||||||||||||
23 TTGGAGCAATAA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 ttggagcaataa 70
||||||||||||
23 TTGGAGCAATAA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity hes 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 30,518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
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(415)324-1678
                                                                                                                               ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.3%;
                                                                                                                            13.3%; Score 12; DB
100.0%; Pred. No. 2.
Live 0; Mismatches
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er 10, 1995
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; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Lo
                                                                                                                                                                  DB 3;
                                                                                                                                                 2.1e+03;
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                                                                                                                                                             Length 23;
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US-08-210-762E-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)415-0100
TELEFAX: (703)418-2768
INFORMATION FOR SEQ ID NO: 31:
                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/120,096
FILING DATE: 13-SEP-93
APPLICATION NUMBER: 08/111,519
FILING DATE: 25-AUG-93
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                   PUBLICATION INFORMATION:
AUTHORS: Hjelle, Brian
AUTHORS: Jenison, Stev
                                                                                                                                                                                                                                                                                                                                                           INDIVIDUAL ISOLATE: 3H226 IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: Accel 486
OPERATING SYSTEM: Windows 3.1
SOFTWARE: WordDerfect 6.1 for Windows
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch, 500 Kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: cDNA viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hjelle, Brian APPLICANT: Jenison, Stev
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                                                                                                                                                                                                                               AUTHORS:
                                                                                                                                                          AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
FILING DATE: 22-MAR
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Buttmi, Jean A.
REGISTRATION NUMBER: 24,236
                                                                                                                                                                                              AUTHORS:
                                                                                                                                                                                                                                                                                                                       CLONE:
                                                                                                                                                                                                                                                                                                                                            LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08 FILING DATE: 26-OCT-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U
ZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Arlington
STATE: Virginia
                RELEVANT RESIDUES IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
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                               in press
1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
                                                                                                 A NO. 5837441el Hantavirus Associated with an Outbreak of Fatal Respir Disease in the Southwestern United States: Evolutionary Relationships Hantaviruses-Running Title: Hantavirus-associated ARDS
                                                                     68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Hoffman, Wasson & Gitler
2361 Jefferson Davis Highway
                                                                                                                                                                                                         Torrez-Martinez, No. Yamada, Takashi
No. 5837441te, Kurt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                       Zumwalt, Ross
MacInnes, Kersti
Myers, Gerald
                                                                                                                                                                                                                                                                     Jenison, Steven
                                                                                   Journal
                                                                                                                                                                                                                                                                                                                                                                                              Four Corners Hantavirus
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                                                                                   of Virology
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                SEQ
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                ID
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                NO:
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                1:FROM 1 TO
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Query Match

DB 2; Length 24;

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US-08-462-437-26
; Sequence 26, Applicat
; Patent No. 6232094
; GENERAL INFORMATION:
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US-08-256-799-26
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                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                  Matches
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, v
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,799
FILING DATE: 06-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 88/92
FILING DATE: 23-JAN-1992
ATTONNEY/AGENT INFORMATION:
NAME: COOPER, IVER P.
                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 202-737-3528 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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APPLICANT:
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TITLE OF INVENTION: DNA ENCODING KAPPA-CASEIN, PROCESS FOR
TITLE OF INVENTION: OBTAINING THE PROTEIN AND USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
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APPLICANT: HANSSON, Lennart
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                                                                                                                     12
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TOPOLOGY: lin
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                                                                                                                                                                                                                                                                                                                          TYPE:
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ZIP: 20004
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                                                                                                                     TTATGTTTTCAT 23
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                                           Application US/08462437
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                                                                                                                                                                                                                                                                                                                                   24 base pairs
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Toernell, Jan
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                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                                          DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
                                                                                                                                                                                                                                                                                                        single
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                                                                                                                                                                                             13.3%; Score 12; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      us/08/256,799
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                                                                                                                                                                                Mismatches
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                                                                                                                                                                                             DB 4; L
. 2.1e+03;
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; TOPOLOGY: linear; MOLECULE TYPE: DNA US-08-462-437-26
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US-08-271-880A-140/c
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                                                                                                                                                                                                                                                                                                                         Sequence 140,
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/462,437
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 88/92
FILING DATE: 23-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVET P. 00 005
                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                APPLICANT: James McSwiggen
APPLICANT: Dan T. Stinchcomb
APPLICANT: James D. Thompson
TITLE OF INVENTION: METHOD AND REAGENT FOR INHIBITING
TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS
TITLE OF INVENTION: REPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: TOERNELL, Jan
APPLICANT: TOERNELL, Jan
APPLICANT: TOERNELL, Jan
TITLE OF INVENTION: DNA ENCODING KAPPA-CASEIN, PROCESS
TITLE OF INVENTION: FOR OBTAINING THE PROTEIN AND USE THEREOF
NUMBER OF SEQUENCES: 31
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth S
STREET: Suite 4700
CITY: Los Angeles
STATE: California
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                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                 NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12; Conservative
                                                                                                                                                                                                                                                                                                      40, Application US/08271880A 5693535
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                                                                                                                                                                                                                                                                   Kenneth G. Draper
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                                                                                                                 REPLICATION 232
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100.0%; Pred. No. 2.1e+03
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SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-271-880A-140
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PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA: including appplication
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/103,243
FILING DATE: August 6, 1993
APPLICATION NUMBER: 07/882,886
FILING DATE: May 14, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 206/116
FELECOMMUNICATION: INFORMATION:
TELEFAX: (213) 489-1600
TELEFAX: (213) 489-1600
TELEFAX: (213) 955-0440
INFORMATION FOR SEO ID NO: 140:
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Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 140, Application US/08910408 Patent No. 5972704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                               COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: James McSwiggen
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McThon
APPLICANT: James J. Thompson
TITLE OF INVENTION: METHOD AND REAGENT FOR INHIBITING
TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS
TITLE OF INVENTION: REPLICATION
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM: IBM P.C. DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/271.
FILING DATE: July 7, 1994
                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Apport
                                                                                                                                                                                                                                                                                                                                            STATE: C
APPLICATION NUMBER:
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Bharat Chowrira
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100.0%; Pred. No. 2.1e+03;
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US/08/910,408
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RESULT 31
US-09-249-215-140/c
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Patent No. 6159692
GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08
FILING DATE: July 7, 1
APPLICATION NUMBER: 08
.FILING DATE: August 6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 20 TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 07/88:
FILING DATE: May 14, 1992
ATTORNEY/AGENT INFORMATION:
PRIOR APPLICATION DATA: 08/910,408
APPLICATION NUMBER: 08/910,408
EILING DATE: <UNKNOWN>
APPLICATION NUMBER: 08/103,243
EILING DATE: August 6, 1993
APPLICATION NUMBER: 07/882,886
FILING DATE: May 14, 1992
ATTORNEY/AGENT INFORMATION:
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TELEFAX: (213) 955-0440
TELEX: 67-3510
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Dan T. Stinchcomb
James D. Thompson
TITLE OF INVENTION: METHOD AND REAGENT FOR INHIBITING
HUMAN IMMUNODEFICIENCY VIRUS
                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,215
FILING DATE: 12-Feb-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
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OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ Version 1.5
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STATE: California
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US-08-835-728D-72
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Query Match
Best Local Similarity
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Best Local
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                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
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                                                                               TOPOLOGY: li
                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                             APPLICATION NUMBER: 08/656,716
FILING DATE: June 03, 1996,
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/125001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOETWARE: PATENTIN Release #1.0/
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 92037
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 42...
STREET: 42...
CITY: La Jolla
CTATE: CA
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                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/835,728D FILING DATE: April 11, 1997 CLASSIFICATION: 435
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                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                 TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (213) 955-0440 TELEX: 67-3510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 206/116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Warburg, Richard REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Fish & Richardson P.C. 4225 Executive Square, Suite 1400
                                                                                                                                                                                                 619/678-5070
619/678-5099
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                                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn Release #1.0, Version #1.30
                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.3%; sc.
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Methylation Specific Detection
 13.3%;
 Score 12;
Pred. No.
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Pred. No.
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2.1e+03;
 DB 3; L
2.1e+03;
               Length 26;
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US-08-835-728D-176/c: Sequence 176, Application US/08835728D; Patent No. 6017704; GENERAL INFORMATION:
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                                                                                                                                                                       US-09-490-558-72
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Matches
                                                                                                                                      Sequence 72, Application US/09490558 Patent No. 6265171
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/835,728D
FILING DATE: APFil 11, 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                      GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
NUMBER OF SEQUENCES: 216

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 4225 Executive Square, Suite 1400
                                                   APPLICANT: Herman, James G.
APPLICANT: Baylin, Stephen B.
TITLE OF INVENTION: Methylation Specific Detection
NUMBER OF SEQUENCES: 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Herman, James G. APPLICANT: Baylin, Stephen B. TITLE OF INVENTION: Methylati
                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/61
FILING DATE: June 03, 19
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Lisa A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                        21 TTTTATGTTTT 10
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                                                                                                                                                                                                                                                                                                          Local Similarity
mes 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: UZIP: 92037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: La Jolla
STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER:
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STREET: 4225 Executive Square,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH:
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3, 1996,
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0; Mismatches
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e, Suite 1400
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COUNTRY:

USA

Jolla

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Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 6265171
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 0726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Herman, James G. APPLICANT: Baylin, Stephen B. TITLE OF INVENTION: Methylati
                                                                      PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32 tttttatgtttt 43
NAME: Haile, Lisa A. REGISTRATION NUMBER: 38,347
                                                      FILING DATE:
                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                  STREET:
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                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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:: CA
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                                                                                                                                                                                                                                                                                                                                                                                                       Methylation Specific Detection
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                                                                      08/835,728
                                                                                                                                      US/09/490,558
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hes 0;
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Query Match

13.3%;

Score 12;

DB 2;

Length 27;

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RESULT 36
US-08-668-128B-6/c
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; MOLECULE TYPE:
US-09-490-558-176
US-08-668-128B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/08668128B Patent No. 5840568
                                                               TELEFAX: (212) 838-388
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
                                                                                                                                                                                      PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/580,980
FILING DATE: 03-JANUARY-1996
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/479,328
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:

NAME: Hanson, NO. 5840568man D.

REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 619/678-5099 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/668,128B FILING DATE: 21-JUNE-1996 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/644,116 FILING DATE: 10-MAY-1996
                                                                                                                                                     REFERENCE/DOCKET NUMBER: LU
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Hodg)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 tttttatgtttt 43
                                TYPE: nucleic acid
STRANDEDNESS: sing
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T: 805 Third Avenue
New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New York
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                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM
                                                                                                                                      (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diskette, 3.5 inch, 360 kb storage
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                                                                                                                    838-3884
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; Pred. No.
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RESULT 38
US-08-644-116A-6/c
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Sequence 6, Application US/08644116A Patent No. 6140464 GENERAL INFORMATION:
                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/08905445
Patent No. 5864015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100 Matches 12; Conservative
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CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/905,445
FILING DATE: 04-AUG-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/668,128
FILING DATE: 21-JUNE-196
APPLICATION UNMBER: 08/644,116
FILING DATE: 10-MAY-1996
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                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212) 838-3884
NFORMATION FOR SEQ ID NO: 0
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Hanson, No. 5864015man D. REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 54
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Pfreundschuh, Michael
TITLE OF INVENTION: Hodgkin's Disease Associated Molecules And
TITLE OF INVENTION: Uses Thereof
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/580,980 FILING DATE: 03-JANUARY-1996 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/479
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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STREET: 8(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New York City
STATE: New York
ZIP: 10022
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                                                                                                                                 26 TGAAAGCAAGTG 15
                                                                                                                                                    77 tgaaagcaagtg 88
                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77 tgaaagcaagtg 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Felfe & Lynch
805 Third Avenue
                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diskette, 3.5 inch, 360 kb storage
                                                                                                                                                                                                     13.3%; Score 12;
100.0%; Pred. No.
tive 0; Mismatc
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. 2.1e+03;
                                                                                                                                                                                                                                         Length 27;
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US-08-771-602D-20
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TELEPAX: (214)
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
Description
TRUGTH: 27 base pairs
                                                                                                                                                                                                                                                                                                                                                     Sequence 20, Application US/08771602D Patent No. 5976795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/580,980
ETLING DATE: 03-JANUARY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,328
ETLING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6140464man D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: 10-MAY-1996
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                     TITLE OF INVENTION: Re-
NUMBER OF SEQUENCES: 5:
CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: Method For Identifying Or Isolat
TITLE OF INVENTION: And Molecules Identified Thereby
                                                                                                                                                                                                                                                                                               APPLICANT: Voytas, Daniel F. APPLICANT: Zou, Sige
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                ADDRESSEE: Greenlee, Winner and Sullivan, P.C. STREET: 5370 Manhattan Circle, Suite 201 CITY: Boulder CITY: Boulder STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: UZIP: 80303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: sing
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STATE: New York
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 APPLICATION NUMBER:
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10022
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WENTION: Method For Identifying Or Isolating A Molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (212) 838-3884
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10-MAY-1996
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 US/08/771,602D
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PRIOR APPLICATION DATA:

FILING DATE: 20 CLASSIFICATION:

20-DEC-1996

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; HYPOTHETICAL:
US-08-771-602D-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-771-602D-21/c
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Best Local Similarity 100
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 21,
                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/010,869
FILING DATE: 31-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Perber, Donna M.
REGISTRATION NUMBER: 3,878
REGISTRATION NUMBER: 8-96
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
                                                                      TELEFAX: (303) 499-80 INFORMATION FOR SEQ ID NO:
              SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Retrotransposon and Methods
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Voytas, Daniel F. APPLICANT: Zou, Sige
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "Oligonucleotide."
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 5370 M
CITY: Boulder
STATE: Colorad
                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/771,602D FILING DATE: 20-DEC-1996
                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31 atttttatgttt 42
STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
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5976795
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                                                                                     (303) 499-8089
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                                                                                                      (303) 499-8080
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31-JAN-1996
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Pred. No.
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2e+03;
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RESULT
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US-08-619-724-3/c
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; HYPOTHETICAL:
US-08-771-602D-21
                                                                                              Query Match
Best Local Similarity
Matches 12; Conserv
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Matches 12; Conserv
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                                                                                                                                                                                                                                                                      APPLICATION NUMBER: GB 9319826.5 FILING DATE: 23-SEP-1993 INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SAMMES, FELE CULT.
APPLICANT: GARMAN, Andrew John
APPLICANT: TOP INVENTION: NUCLEIC ACID DETECTION WITH ENERGY TRANSFER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Oligonucleotide."
                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9
FILING DATE: 16-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB94/02068
FILING DATE: 23-SEP-1994
                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                            .26 ctgtaattttta 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Microsoft Word
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/619,724 FILING DATE: 20-MAY-1996
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                                            29 CTGTAATTTTA 18
                                                                                                                                                                                                             LENGTH: 30 base pairs TYPE: nucleic acid STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                      Conservative
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2e+03;
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. 2e+03;
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                                                                                                                                   Length 30;
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US-08-629-001A-25/c; Sequence 25, Application US/08629001A; Patent No. 585861; GENERAL INFORMATION:

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; OTHER INFORMATION: Description of Artificial Sequence:intronic
; OTHER INFORMATION: sequence
US-08-642-274D-104
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APPLICANT: Shiloh, Yosef
TITLE OF INVENTION: MUTATED FORMS OF THE ATAXIA-TELANGIECTASIA GENE AND METHOD TO
TITLE OF INVENTION: SCREEN FOR A PARTIAL A-T PHENOTYPE
                          Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                            SEQ ID NO 104
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 104, Application US/08642274D Patent No. 6200749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local Similarity
                                                                                                                                                                                                                                                    FILE REFERENCE: 229000033
CURRENT APPLICATION NUMBER: US/08/642,274D
CURRENT FILING DATE: 1996-05-03
NUMBER OF SEQ ID NOS: 220
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (810) 539-5055
INFORMATION FOR SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: 2290
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810) 539-5050
                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                        LENGTH: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Shiloh, Yosef TITLE OF INVENTION: ATAX TITLE OF INVENTION: GENO
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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4 aaaaaaaattatt 15
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30500 No. 5858661thwestern Hwy
                                 Conservative
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SYSTEM: PC-DOS/MS-DOS
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                                                   Score 12;
Pred. No.
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2e+03;
                                 0; Indels
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US-08-935-312-14/c
US-08-935-312-14/c
Sequence 14, Application US/08935312
Patent No. 6207455
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APPLICANT: CHANG, Lung-Ji
                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                         APPLICANT: MOORE, Malcolm A.S.
TITLE OF INVENTION: COMPOSITIONS OF SOLUBLE C-KIT LIGAND AND
TITLE OF INVENTION: HEMATOPOIETIC FACTORS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = ""DNA""
                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, Iver P.
REGISTRATION NUMBER: 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
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ADDRESSEE: BROWDY AN
                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
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                                            STREET:
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CITY: Washington
STATE: D.C.
COUNTRY:
                            CITY: New York
                                            ADDRESSEE: Cooper & Dunham LLP STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                      28 CAATGAAAGCAA 17
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les 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
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              New York
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                                                                                                                                                        No. 5767074ka, Karl
Buck, Jochen
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                                                                                                                                                                                        Besmer, Peter
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N: 435
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/341,456A
FILING DATE: 17-NOV-1994
CLASSIFICATION: 514
AATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 37454-C1
TELEPONUNICATION INFORMATION:
TELEPAN: (212) 391-0525
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
TOPOLOGY: unknown
NOLECULE TYPE: DNA (genomic)
US-08-341-456A-14
                                                                                                      В
Search completed: January 24, 2002, 03:24:26 Job time: 3713 sec
                                                                                                                                                                               Query Match 13.3%; Score 12; DB 1; Length 33; Best Local Similarity 100.0%; Pred. No. 2e+03; Matches 12; Conservative 0; Mismatches 0; Indels
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                                                               Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTAt 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
                        Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucel sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
                                                                                                                                                                                                          Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                  l (bases 1 to 50)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
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T. brucei sheared genomic
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AZ42304 IM03020010
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AZ766483 1M054A10

AZ387817 1M0147B24

AL482984 T. brucei

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2M0107124F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0107124 F, DNA sequence.
AZ829725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0107 row: I column: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: CGTTGTAAAACGACGGCCAGT Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
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University of Utah
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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was blunt end-repaired with T4 DNA polymerase and T4 polynucleotides kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AFT129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biomedical
                                                                                                                                                                                                            /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PW042nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                      (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="154f10"
7 c 9 q 14 t
                                                                                                                                                                                                                                                                                           /clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
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/clone="UUGC2M0107I24"
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                                                                                                l Similarity
13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is 4 kb). The v + i method used for the library construction is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucel genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TA123B120 26 bp DNA GSS 13-DEC-2000 T. brucei sheared genomic DNA clone 123b12, reverse sequence, genomic survey sequence.
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13; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre
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                                                                                                                                                                                                                                                                                                                                                                                                                           at http://www.sanger.ac.uk/Projects/T_brucei/
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                                                                                                                                                                                                                                                                                                                           /organism="Trypanosoma
/strain="TREU927"
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/clone="123b12"
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13; Conserv
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Insert Length: 10000 Std Error: 0.00
Plate: 0252 row: E column: 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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/clone="UUGC1M0252E07"
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/strain="C57BL/6J"
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13; Conserv
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University of Utah
Rm. 308, Biomedical
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Fax: 801 585 7177
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Islam,H., Longacre,S.; Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="E. Coli strain XL10-Gold, T1-resistant, F
/note="Vector: PWD42nv; Purified genomic DNA from M.
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/clone="UUGC1M0030N24"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA500776 49 bp mRNA EST 01-JUL-1997 vg01b11.rl Soares mouse NbMH Mus musculus cDNA clone IMAGE:860061 5' similar to TR:G1333638 G1333638 PARAOXONASE 2. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Ld
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trace considered overall poor quality Possible reversed clone: similarity on wrong strand Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus".
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:860061"
/clone=lib="Soares mouse NbMH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="heart"
/dev_stage="4 weeks"
/lab_host="DH10B"
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Contact: Robert B. W
University of Utah G
University of Utah
                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0367 row: N column: 03
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                        Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-NaKagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
                                                                                                                             Tel: 801 585 5606 Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                   Mouse whole genome
                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria;
1 (bases 1 to 23)
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Department of Virology
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Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries
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1 (bases 1 to 50)
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13 c 8 g 10 t
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/clone="CAS10730"
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                                         Email: ddunn@genetics.utah.edu
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1 (bases 1 to 24)
1 (bases 1, bases, Mamoud, M., Beacorn, T., Duval, B., Hamil, C. Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AZ996858 24 bp DNA 2M0283L08F Mouse 10kb plasmid UUGC2M library Mus clone UUGC2M0283L08 F, DNA sequence.
                                                                                                                                                                                      Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Res
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                          Plate: 0283 row: L column: 08
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                                                                                                                                                                                                                                                                                                                                                   ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
Class: plasmid ends
                                                                                                                  Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                  Unpublished (2000)
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100.0%;
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                  Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0080 row: E column: 2
                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                            Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Isian, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rei, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
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Location/Qualifiers
                                                                                                                                                                            University of Utah University of Utah
                                                                                                                                                                                                                        Contact: Robert B.
                                                                                                                                                                                                                                             Unpublished (2000)
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1 (bases 1 to 25)
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Mammalia; Eutheria; Rodentia;
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/note="Vector: PW042nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
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/clone="UUGC2M0283L08"
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Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washingtion Genome Center. Vector Trimming: cross_match from University of Washingtion Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washingtion Genome Center. http://www.genome.washington.edu Low Quality Sequence: 10
                                                                                                                                                                                                                                                                                                                Unpublished (1999)
Other_ESTs: 2821693.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA sequence.
AW246455
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High quality sequence stop: 25.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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1 (bases 1 to 27)
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/clone="UUGC1M0080E20"
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o. 2.8e+05;
0;
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RESULT 1
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                    Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhaus Mouse whole France, R., Mouse whole France, R.
                                                                        Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0435 row: E column: 23
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                          plasmid inserts
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria;
1 (bases 1 to 30)
Dunn, D., Aoyagi, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1M0435E23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0435E23 R, DNA sequence.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peaks following vector sequence. Polyadenylation: Based upon the presence of a KhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was
                    High quality sequence stop: 30.
Location/Qualifiers
                                                                                                                                                        Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                  University of Utah
University of Utah
                                                                                                                                                                                                                                                                                                                                  Mouse whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
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                                                            Class: plasmid ends
                                                                                                                                                                                              84112,
                                                                                                                                                                                                                                                                          Contact: Robert B.
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Plate: LLCM7 r
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           house mouse.
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                                                                                                                                                                                                USA
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                                                                                                                                                                                                                Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="NIH_MCC_7"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2821693"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="DH10B (phage-resistant)"
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Pred. No.
                                                                                                                    Std Error: 0.00
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. 2.7e+05;
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/organism="Mus musculus' /strain="C57BL/6J"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/clone="UUGC1M0435E23" /db_xref="taxon:10090"

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FEATURES
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AZ507698
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                  unn,D.; Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
                                                                                                     Email: ddunn@genetics.utah.edu
Insert Length: 1,0000 Std Error: 0.00
Plate: 0349 row: 0 column: 21
                                                                                                                                                                                                                                                                           Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 33)
                         High quality sequence stop: 33
                                                                                                                                                                              Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                 plasmid inserts
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                                                                           Seq primer: CGTTGTAAAACGACGGCCAGT
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                                                   lass: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance. a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of publase (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and constituted with adaptors complementary to the insert adaptors and
                                                                                                                                                                                                                                                    Biomedical Polymers Research Bldg.,
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (http://www.jax.org/resources/documents/dnares/). The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory Mouse DNA Resource
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Pred. No. 2.6e+05;
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RESULT 14
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                                                                  Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0316 row: A column: 18
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12; Conserv
Class: plasmid ends .
High quality sequence stop: 38.
                                                                                                                                        Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                              Contact: Robert B.
University of Utah
University of Utah
                                                                                                                                                                                                                                                                                                     Unpublished (2000)
                                                                                                                                                                                                                                                                                                                           plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
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                                             Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                Mouse whole genome
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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308, 1
308, 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWDA2 (gi14732114 gblAF129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coil xL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                           Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (http://www.jax.org/resources/documents/dnares/). The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="mouse 10kb plasmid UUGC1M library"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="UUGC1M0349021"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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                                                                                                                                                                                                                                                        Genome Center
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Pred. No.
                                                                                          Std Error: 0.00
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2.5e+05;
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REFERENCE
AUTHORS
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AZ662545/c
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26 TGAAAAAAATTA 37
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                                                                         Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0541 row: P column: 07
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1M0541P07R Mouse 10kb plasmid UUGC1M library Mus musculus
clone UUGC1M0541P07 R, DNA sequence.
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                     University of Utah Genome Center University of Utah
                                        Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                     Rm. 308,
                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly, Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa;
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/clone="UUGC1M0316A18"
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100.0%; Pred. No. .
'The 0; Mismatches
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Rodentia;
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. 2.4e+05;
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RESULT 1
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
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                                                                                                                                                                                                                                                                      Burns,N., Grimwade,B., Ross-Macdonald,P.B., Choi,E.-Y., Finberg,K., Roeder,G.S. and Snyder,M.
Large-scale analysis of gene expression, protein localization and gene disruption in Saccharomyces cerevisiae
Genes Dev. 8, 1087-1105 (1994)
95011603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T17635
T17635.1
                                                                                                                                                                           Department of Biology
Yale University
New Haven CT 06520-8103
                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T17635 42 bp
mps v360 The blue guy
sequence upstream of
pattern:
50 cytoplasmic spots; Disruption phenotype: none detected; Fusion:
codon 407 of GAC1 gene. Sequence below near or adjacent to lac2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST
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Location/Qualifiers
                                                                                                                                                                                                                                                Contact: Snyder M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              baker's yeast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence.
                                                                                                           Email: snymicp@yalevm.ycc.yale.edu
                                                                                                                                                       Tel: 2034326139
                                                                                LacZ fusion; Vegetative expression; Beta-gal fusion localization
                                                                                                                                 Fax: 2034326161
                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 42)
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/strain="C57BL/6J"
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100.0%; Prr
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Pred. No.
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RESULT 17
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                                                                                                             High quality sequence stop: 45
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AZ514394 45 bp DNA GSS 05-OCT-2000 1M0361J02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0361J02 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
                                                                                                                                                                              Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0361 row: J column: 02
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 45)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
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                                                                                                                                                                                                                                                                             Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                              Biomedical Polymers Research Bldg., 20 S.
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0361J02"
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/lab_host="E.coli"
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12; Conser
                                                                                                                                                                                                                                                                                                                                                                   IMAGE Consortium (info@image.llnl.gov) for further
Trace considered overall poor quality
Insert Length: 606    Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-femail.nih.gov
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 46)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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                                                                                                                                /clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
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/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                 /clone="IMAGE: 2090356"
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AZ832106 48 bp DNA GSS 20-FEB-2 2M0112113F Mouse 10kb plasmid UUGC1M library Mus musculus clone UUGC2M0112113 F, DNA sequence.
AZ832106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 801 585 5606 Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
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Length: 10000 Std Erro
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel
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                                                                                                                                                                                                              /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0112I13"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
                                                                                                                                                                                             Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                         /sex="Male"
                                                                                                                                                                                                                                                              /lab_host="E. Coli strain XL10-Gold, T1-resistant,
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                 AZ782616 20 bp DNA GSS 16-FEB-2001 2M0023F17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0023F17 R, DNA sequence.
AZ782616
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Institute for Molecular and Cellular Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ,H., Arimoto,J: and Matsubara,K.

Gene expression of human promyelocytic cell line HL60 before and after induction of differentiation. A new application of 3'directed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1993)
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Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                 promyelocyte.
                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Human promyelocyte"
/note="Female, adult, cell_line
promyelocyte. "
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/db_xref="taxon:9606"
/clone="mm06d08"
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AL/188088 21 bp DNA GSS 16-FEB-2001 1M0567G21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0567G21 R, DNA sequence.
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University of Utah Genome Center
University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
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Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
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/clone="UUGC2M0023F17"
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0. 8.8e+05;
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RESULT 23
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11; Conserv
AA991150 22 bp mRNA EST 03-JUN-1998 os40a07.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1607796 3' similar to TR:Q35990 Q35990 HYPOTHETICAL 8.9 KD PROTEIN.; contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0567 row: G column: 21
Seq primer: CACACAGGAAACAGCTATGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 801 585 5606
Fax: 801 585 7177
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jack
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/strain="C57BL/6J"
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/clone="UUGC1M0567G21"
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                          Mammalia; Eutheria; Rodentia; 1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                             AZ766483 22 bp DNA GSS 16-FEB-2001 1M0564A10F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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Location/Qualifiers
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Contact: Robert Strausberg, Ph.D.
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 {\tt AA991150}
               Islam,H.,
                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                      Mus musculus
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National Cancer Institute, Cancer Genome Ana
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/db_xref="taxon:9606"
/clone="IMAGB:1607796"
/clone_lib="NCI_CGAP_Br2"
/sex="female, pooled"
/tissue_type="breast"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Wector: pT7T3D-Pac (Pharmacia) with a modified /note="Wector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pooled bulk breast tumor tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. This library is the normalized version of NOI_CGAP_BT1.1 Library was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and M. Fatima Bonaldo.
3 c 2 g
        Aoyagi,A., Barber,M., Beacorn,T., Duv
Longacre,S., Mahmoud,M., Meenen,E.,
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. 8.5e+05;
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                                 Duval, B., Hamil, C.
           Pedersen, T., Reilly
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                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 23)
                                                                                                                                                                                                   1M0147B24R Mouse 10kb plasmid UUGC1M library Mus
clone UUGC1M0147B24 R, DNA sequence.
Dunn, D.,
                                                                                       Mus musculus
                                                                                                                                      GSS
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University of Utah Genome Center
University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0564 row: A column: 10
Seq primer: CGTTGTAAAACGACGGCCAGT
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pNBM2 (9i14732114)phAF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
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Aoyagi, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."

2 c 4 g 12 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /SeX="Male" /SeX="Male" Coli strain XL10-Gold, Ti-resistant, F
/Lab_host="E. Coli strain XL10-Gold, Ti-resistant, F
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/strain="C57BL/6J"
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                                                                                                                                                           GI:10501525
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Barber, M.,
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Pred. No. 8.5e+05;
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Beacorn, T.,
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Duval, B.,
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T. brucei sheared genomic DNA clone 242f03,
genomic survey sequence.
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Insert Length: 10000 Std Erro
Plate: 0147 row: B column: 2
                                                                     Trypanosoma brucei
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  Trypanosoma.
1 (bases 1 to 24)
                                            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                          Trypanosoma brucei.
                                                                                                                                    AL482984.1 GI:11848725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
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and selected for ampicillin resistance."
4 c 3 g 11 t
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/clone="UUGC1M0147B24"
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/strain="C57BL/6J"
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M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
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High quality sequence stop: 25.
Location/Qualifiers
                                       Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0269 row: P column: 09
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 1 (bases 1 to 25)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1M0269P09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0269P09 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Constructed at the institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucel genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
                                                                                                                                                       Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                University of Utah Genome University of Utah
                                                                                                                                                                                                                                                                                                                                                                                  ,M., Rose,M., Rose,R., and Wright,D.,Weiss,R.
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                                                                                                                                                                                                                                                                                              Contact: Robert B.
                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                           plasmid
                                                                                                                                                                                                                                                                                                                                                             Mouse whole genome scaffolding with paired end reads from 10kb
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/strain="TREU927"
/db_xref="taxon:5691"
/clone="242f03"
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Pred. No.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
                                                      Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0073 row: I column: 20
                                                                                                                                                                            University of Utah (University of Utah Rm. 308, Biomedical
                                                                                                                                                                                                                                       Unpublished (2000)
Contact: Robert B.
                                                                                                                                                                                                                                                                                                                     Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
High quality sequence stop: 28
                     Class: plasmid ends
                                   Plate: 0073 row: I column: 20
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (http://www.jax.org/resources/documents/dnares/). The DNA
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Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Kawamoto, S., Okubo, K., Yoshii, J., Katsuki, M. and Matsubara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               \label{eq:Kawamoto,S.} \begin{tabular}{ll} Kawamoto,S., & Okubo,K., & Yoshii,J., & Katsuki,M. & and & Matsubara,K. \\ Analysis of gene expression in mouse embryogenesis by $3'$-directed \\ \end{tabular}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 29)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Institute for Cellular and Molecular Biology
                                                                                                                                                                                                                                                                                                                                                                                                            Yamada-oka, Suita, Osaka
Location/Qualifiers
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jack
/clone_lib="Mouse 3'-directed"
/tissue_type="decidual tissue (day 6.5-8.5 of gestation)"
3 c 2 g 9 t
                                                                                                                                                                 /db_xref="taxon:10092"
/clone="md0169"
                                                                                                                                                                                                                                                               /organism="Mus musculus domesticus"
/strain="C57BL/6J"
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone="UUGC2M0073I20"
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Best Local
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1 (bases 1 to 29)

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University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Err
Plate: 0368 row: G column: 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1M0368G02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0368G02 R, DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 801 585 5606
Fax: 801 585 7177
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ580321.1 GI:11694750
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                                                                                                  10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwb42 (gil473214) gblaF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="mouse 10kb plasmid UUGClM library"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="UUGC1M0368G02"
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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Pred. No. 7.7e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0363 row: N column: 13
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D.,Weiss,R.
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1 (bases 1 to 31)
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                                                              (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pHSD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
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adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance.
                                                                                                                                                                                                                                                                                                                                                                                              musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Mouse 10kb plasmid UUGC1M library"
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0059 row: P column: 11
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Seq primer: CACACAGGAAACAGCTATGACC
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University of Utah Genome Center
University of Utah
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AZ331642.1 GI:10394528
GSS.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                          10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AFR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                       was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                        (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA
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  chemically-competent E. coli
                           adaptored vector DNA, and transformed into
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/note="Vector: PWD42nv; Purified genomic DNA from M.
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/clone="UUGC1M0059P11"
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/strain="C57BL/6J"
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| 20 ATTTCAAAGTT 10
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Insert Length: 10000 Std Error:
Plate: 0402 row: F column: 21
Seg primer: CGTTGTAAAACGACGGCCAGT
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University of Utah
University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
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            was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                          (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0402F21"
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  adaptored vector DNA, and transformed into
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U44209
 Mus musculus
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Quantitative analysis of gene expression in sexual structures
Aspergillus nidulants by sequencing of 3'-directed cDNA clones
FEMS Microbiol. Lett. 138 (1), 71-76 (1996)
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

Eurotiales; Trichocomaceae; Emericella.

1 (bases 1 to 33)
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               nouse mouse.
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/tissue_type="cleistothecium"
/cell_type="Hull cell"
/dev_stage="sexual"
/note="3'-directed cDNA clones; single-pass sequencing"
a C 2 g 10 t
                                                                                                                                                                                                                                                                                                                                                                      /organism="Emericella nidulans"
/strain="FGSC4"
/db_xref="faxon:162425"
/clone="SE0393"
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clone UUGCIM0329F05 R, DNA sequence.
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University of Utah
University of Utah
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1 (bases 1 to 33)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 33.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|473214|gb|AB129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory Mouse DNA Resource
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/clone="UUGC1M0202010"
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; Pred. No. 7.4e+05;
0; Mismatches 0;
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M., Meenen,E., Pedersen,T., Reilly
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                    Schizosaccharomyces pombe cDNA clone spc09897, mRNA sec AU014463 AU014463.1 GI:3369254
                                                                               AU014463 35 bp mRNA EST AU014463 Schizosaccharomyces pombe late log
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0329 row: F column: 05
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,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Res
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
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1 (bases 1 to 33)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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/clone="UUGC1M0329F05"
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/strain="C57BL/6J"
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7.4e+05;
hes 0;
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1 (bases 1 to 35)

Okubo,K., Fukushima,A., Yoshii,J., Niiyama,T., Kojima,Y., Yoshinari,H., Arimoto,J. and Matsubara,K.

Gene expression of human promyelocytic cell line HL60 before and after induction of differentiation. A new application of 3'directed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l Similarity
11; Conserv
                                                                                                                                                                                                            Institute for Molecular and Cellular Biology Osaka University
                                                                                                                                                                                                                                                                           Unpublished (1993)
Contact: Okubo, K., Fukushima, A., Yoshii, J., Niiyama, T., Kojima, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUMGS00963 Human promyelocyte Homo sapiens cDNA clone mp1322 3',
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Genome Research Group
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Morinyo,M. and Mita,K.
Identification of expressed sequence tags of Schizosaccharomyces
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9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fission yeast.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            morimyo@nirs.go.jp.
Location/Qualifiers
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                                  /db_xref="taxon:9606"
/clone="mp1322"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schizosaccharomyces pombe was prepared by cloning cDNA into the Smal site of Ml3mpl9 DNA and the direction of DNA sequences was not always from 5′ to 3′. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)" 1 c 5 g 8 t
/clone_lib="Human promyelocyte"
/note="Female, adult, cell_line = HL60, cell_type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="spc09897"
/clone_lib="Schizosaccharomyces pombe late log
/sex="h minus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Schizosaccharomyces pombe"
/strain="972"
                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GI:500892
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hes 0;
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Best Local
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Best Local
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                                                                                                          AZ381596 36 bp DNA
1M0138C16F Mouse 10kb plasmid UUGCIM library Mus musculus clone UUGCIM0138C16 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
. Phahditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUIIII149 36 bp mRNA EST: 19-OCT-2000 AUIIII149 unpublished oligo-capped cDNA library Caenorhabditis elegans cDNA clone yk724e1 5', mRNA sequence.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Biology Lab.
National Institute of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and Sugano, S.
                                                                                             AZ381596.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
                                                           house mouse.
                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yata 1111, Mishima, Shizuoka 411, Tel: 81-559-81-6854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax: 81-559-81-6855
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                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="unpublished oligo-capped cDNA library"
/sex="Hermaphrodite"
/tissue_type="whole animal"
/dev_stage="varied"
3 c 6 g 10 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="N2"
/db_xref="taxon:6239"
/clone="yk724e1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Caenorhabditis elegans"
                                                                                             GI:10495296
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7.2e+05;
hes 0;
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                                                                                                                                                                RESULT 41
AZ807406/c
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                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                               l Similarity
11; Conserv
                                                                                         AZ807406 36 bp DNA GSS 20-FEB-7 2M0070015F Mouse 10kb plasmid UUGC1M library Mus musculus clone UUGC2M0070D15 F, DNA sequence.
AZ807406
                                                     AZ807406.1 GI:12971722
GSS.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                   Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0138 row: C column: 16
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 36)
Dunn, D., Aoyagi, A.,
                                      house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pND42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and with adaptors complementary to the insert adaptors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biomedical
                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 purified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (http://www.jax.org/resources/documents/dnares/). The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="UUGC1M0138C16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                Score 11;
Pred. No.
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0. 7.2e+05;

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20-FEB-2001

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RESULT 4
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SOURCE
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                                                                                                                                                                                                                                                                                           l Similarity
11; Conserv
                                                    ;, mRNA sequence.
AA647854
                                                                                        vq80e05.s1 Knowles Solter mouse IMAGE:1108640 5' similar to TR:G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
   house mouse
                                     AA647854.1
                                                                                                                           AA647854
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: CGTTGTAAAACGACGGCCAGT
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Contact: Robert B.
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1 (bases 1 to 36)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
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801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                  purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114)gblnF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biomedical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Mouse 10kb plasmid UUGC1M library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
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                                     GI:2574283
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                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                          Score 11;
Pred. No.
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                                                                                      A EST 28-OCT-1997 ouse 2 cell Mus musculus cDNA clone TR:G1136390 G1136390 KIAA0164 PROTEIN
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,M., Meenen,E., Pedersen,T., Reilly
                                                                                                                                                                                                                                                                                                        DB 13; I
7.2e+05;
                                                                                                                                                                                                                                                                                                                           Length 36;
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ORGANISM
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Unpublished (1997)
                                                                                                                                                               EST
                  Tumor Gene Index
                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                         Homo sapiens
                                                                                                                                                                              AI200438.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1996)
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                                                                   (bases 1 to 37)
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ORGANISM
                                                                                                                                                                                                                                                      AI200438 37 bp mRNA EST 29-NOV-1998 qf93b01.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1757545 3' similar to SW:QPCT_HUMAN Q16769 GLUTAMINYL-PEPTIDE CYCLOTRANSERASE PRECURSOR ; contains element
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                   MER35 repetitive element;, mRNA sequence. AI200438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Marra M/Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4444 Forest Park Parkway, Box 8501,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Knowles Solter mouse 2
/tissue_type="embryo"
/dev_stage="2-cell"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/strain="B6D2 F1/J"
/db_xref="taxon:10090"
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                                                                       Primates;
                                                                                             Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 11;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                       Craniata; Vertebrata;
Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 10; ; 7.1e+05;
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                                                                         Hominidae;
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                                                                                                Euteleostomi;
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Best Local
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||||||||||||||
                             Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0
Plate: 0069 row: I column: 08
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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Insert Length: 863 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                 Contact: Robert B.
University of Utah
University of Utah
                                                                                                                                                                                                                                      Unpublished (2000)
                                                                                                                                                                                                                                                                                        Dunn,D., Aoyagi.A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longae,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 37)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2m0069108 F mouse 10 kb plasmid UUGC1M library Mus musculus genomic clone UUGC2m0069108 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
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                                                                                                                                                                                                                                                                    Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                            house mouse
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                                                                                                                                                                   308, Biomedical Polymers Research Bldg.,
                 quality sequence stop: 37
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llarity 100.0%;
Conservative (
                                                                                                                                                     USA
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a 6 c 12 g 8 t
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/clone="IMAGE:1757545"
/clone_lib="Soares_placenta_8to9weeks_2NbHP8to9W"
/clone_lib="Soares_placentae: one from 8 weeks and a from 9 weeks post conception"
/lab_host="DH10B (ampicillin resistant)"
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HUMGS02021 Human promyelocyte Homo
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3-1 Yamada-oka,Suita,Osaka 565,Japan.
                                                                                                                                                                                                                                                                                                                                                                    CDNA sequencing
Unpublished (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                        Gene expression of human promyelocytic cell line HL60 after induction of differentiation. A new application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 38)
Okubo, K., Fukushina, A., Yoshii, J., Niiyama, T.,
                                                                                                                                                                                                                                                                                                                   Contact: Okubo,K., Fukushima,A., Yoshii,J., Niiyama,T., Kojima,Y.,
Yoshinari,H., Arimoto,J. and Matsubara,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                           Institute for Molecular and Cellular Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H., Arimoto, J. and Matsubara, K.
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  promyelocyte.
                                   /clone_lib="Human promyelocyte"
/nocte="Female, adult, cell_line = HL60, cell_type
nromvelocyte. "
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/strain="C57BL/6J"
                                                                                                          /clone="mp0144"
                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                            Location/Qualifiers
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Copyright (c) 1993 - 2000 Compugen Ltd
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SUMMARIES

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1 (bases 1 to 26)

Herrnstadt,C. and Davis,R.E.

Single nucleotide polymorphisms in mitochondrial genes that segreg

ate with alzheimer's disease

Patent: WO 0063441-A 43 26-OCT-2000;
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Single nucleotide polymorphisms in mitochondrial genes ate with alzheimer's disease
Patent: WO 0063441-A 13 26-OCT-2000;
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                                                                                                                                   Mutated forms of the ataxia-telangiectasia screen for a partial A-T phenotype Patent: US 6200749 A 158 13-MAR-2001;
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AR011299
AR011299.1 GI:3969289
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1 (bases 1 to 33)
Kearsey,S.
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K01606.1 GI:213953
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/db_xref="taxon:32630"
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Paoletti.E., Perkus, M.E., Taylor, J., Tartaglia, J., Norton, E.K., Riviere, M., de Taisne, C., Limbach, K.J., Johnson, G.P., Pincus, S.E., Cox, W.I., Audonnet, J. Francis and Gettig, R. Robert.
Cox, W.I., Audonnet vaccinia virus and expression vectors thereof Patent: US 576.9938-A 168 09-JUN-1998;
               Thompson, J.D.
HIV nef targeted ribozymes
Patent: US 5972704-A 201 2
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Paoletti, E., Perkus, M.E., Taylor, J., Tartaglia, J., Norton, E.K.,
Riviere, M., de Taisne, C., Limbach, K.J., Johnson, G.P., Pincus, S.E.,
Cox, W.I., Audonnet, J.F. and Gettig, R.R.
NYVAC vaccinia virus recombinants comprising heterologous inserts
Patent: US 5494807-A 168 27-FEB-1996;
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Draper, K.G., Chowr
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                                                                  Stinchcomb, D.T. and
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Draper, K.G., Chowrira, B., McSwiggen, J.,
                                                                                                                                                               Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unknown
                                                                                                      Patent:
                                                                                                                        Thompson, J.D.
                                                                                                                                                                            Unknown.
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Location/Qualifiers
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ent: US 5693535-A 201 02-DEC-1997;
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Habermann, P., Stengelin, S. and Wengenmayer, F.

Rusion proteins, method for their production

Patent: EP 0211299-A 2 25 FEB-1987;
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14-FEB-2001

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BAYER AG
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Bennett, C. Frank, Ackermann, E.J., Swayze, E.E. and Cowsert, L.M.
Antisense modulation of Survivin expression
Patent: US 6077709-A 19 20-JUN-2000;
Location/Qualifiers
1 (bases 1 to 20)
Burnham, M.K. and Hodgson, J.E.
                                                                                                                                                                                                                                                                                                                                                                                                                        artificial sequence.

1 (bases 1 to 20)
Stropp,U., Baumgarten,J., Loebberding,A., Springer,W., Piel,N.,
Stropp,U., Baumgarten,J., Loebberding,A., Springer,W., Piel,N.,
Kretschmer,A., Koelbl,H. and Frommer,W.
Antisense-oligonucleotides for inhibiting the transactivator target sequence (TAR) and the synthesis of the transactivator protein (Tat) of HIV-I, and their use
                                           unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     synthetic construct
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                                                                                                         66 from Patent W09731114.
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/db_xref="taxon:32630"
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                                                         1 (bases 1 to 21)
Nadeau,J.G., Pitner,J.Bruce, Schram,J.L., I and Walker,G.Terrance.
Detection of nucleic acids by fluorescence Patent: US 5846726-A 4 08-DEC-1998;
                                                                                                                                                                                      Sequence 4 from patent AR063857
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12; Conservat
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AR043539
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                                                                                                                                    Unknown
                                                                                                                                                                           AR063857.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amplification and detection of chlamydia trachomatis nucleic acids Patent: US 5814490-A 6 29-SEP-1998;
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AR112325
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AR098733
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Little,M.C. and Vonk,G.P.
Kit and method for fluorescence based detection assay
Patent: US 6077669-A 8 20-JUN-2000;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nadeau,J.G., Pitner,J.Bruce, Linn,C.Preston and Schra
Detection of nucleic acids by fluorescence quenching
Patent: US 5958700-A 4 28-SEP-1999;
Location/Qualifiers
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PD 02-MAR-1998 PP 29-MAY-1998 JP 1998166141
PF 29-MAY-1998 JP 1998166141
PR 30-MAY-1997 US 08/865.675
PI JAMES G NADEAU, J BLUCE PITONA, C PRESTON RIN, JAMES L S C12N15/09, C1201/68, G01N33/50, G01N33/566, C12N15/00 CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/~~~
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Nadeau,J.G., Hsieh,H.V., Pitner,J.Bruce and Linn,C.Preston.
Detection of nucleic acids by fluorescence quenching
Patent: US 613047-A 5 10-CCT-2000;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 21)
James,G.N.J.J., Pitona,C.P.R.R. and L,S.
Method for detecting target nucleic acid sequence and
Patent: JP 1999056380-A 4 02-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA PAT 07-target nucleic acid sequence and
                                                                                                                                                                                                     Length 21;
PAT
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07-FEB-2001
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E33635/c
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                                                                                                                                                                                                                                               Detection of nucleic acid by disappearance of AL Patent: JP 1999155598-A 5 15-JUN-1999;
BECTON DICKINSON & CO
OS Artificial Sequence
PN JP 1999155598-A/5
PD 15-JUN-1999
PF 22-SEP-1000 TO ATTIFICATION OF THE PROPERTY OF THE
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                                                                PI JAMES G NADEAU, HELEN V C,J BLUCE PITONA,C PRESTON RIN PC C1201/68,C07H21/00,C12N15/09,G01N21/64//G01N33/542,G01N33/566, C12N15/00
CC FH Key Location/Qualif:
FT source 1
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OS Unidentified
PN JP 1999123083-A/4
PD 11-MAY-1998 JP 1998
PF 11-MAY-1997 US 08
PI JAMES G NADEAU, J BL
PI GREN P VONG,
PI G TERANSU WALKER
PC C12N15/09, C07H21/0
Strandedness: Single;
CC Topology: Linear;
FH Key
FT Source
FT Source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JP 1999155598-A/5.
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James, G.N.J.J., Pi
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C12N15/09, C07H21/00, C12Q1/68, G01N21/64, G01N33/58, C12N15/00
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II-MAY-1998 JP 1998127068
11-MAY-1997 US 08/855 085
13-MAY-1997 US 08/855 085
JAMES G NADEAU, J BLUCE PITONA, JAMES L SHURAMU, C PRESTON RIN,
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Location/Qualifiers
    /organism="unidentified"
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of nucleic
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5 c 3 g
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OS Artificial Sequence
PN JP 199925799-A/8
PD 24-AUG-199
PF 04-NOV-1998 JP 199831
PR 04-NOV-1997 US 08/
PI MICHAEL C LITTLE, GREN
PC C12Q1/68, G01N21/78, G0
FH Key Locat
FT source 1...2
                                                                                                                                                                   AR037890
Sequence
AR037890
                                       1 (bases 1 to 23)
Gruenert,D.C. and Dohrman,A.F.
Method and assay for detection of the expression
mutations by allele-specific in situ reverse tran
                                                                                                                                                                                                                                                                                                                        l Similarity
12; Conserv
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polymerase chain reaction
Patent: US 5804383-A 10 08-SEP-1998;
Location/Qualifiers
                                                                                                             Unknown
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1 (bases 1 to 21)
Michael,C.L.G.G. and Vong.
Detection assay with the use of fluorescence Patent: JP 1999225799-A 8 24-AUG-1999;
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12; Conser
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                                                                                                  Unclassified
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04-NOV-1997 US 08/964020

MICHAEL C. LITTLE, GREN P VONG

C12Q1/68, G01N21/78, G01N33/50//C12N15/09, C12N15/00

Key Location/Qualifiers
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/db_xref="taxon:32644"
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5 c 3 g
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protein
Patent:
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1 (bases 1 to 24)

1 (bases 1, Stromqvist, M., Bergstrom, S., Hernell, O. and Tornell, J. Hansson, L., Stromqvist, M., Bergstrom process for obtaining the DNA encoding human .kappa. casein and process for obtaining the
                                                                                                                                                                                                                                                           AR151501 24 bp
Sequence 26 from patent
AR151501
AR151501.1 GI:15117551
                                                                                                                                                                                                                           Unknown.
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Hjelle, B. and Jenison, S.
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Sequence 31 from patent US 5837441.
AR054522
AR054522.1 GI:5980099
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Sequence 140 from patent
AR120838
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Draper,K.G., Chowrira,B., McSwiggen,J.,
                                                                                                                                                                                                                                                                                                                                                 Unknown
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Patent: US 5972704-A 140 26-OCT-1999;
Location/Qualifiers
1. 25
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Draper,K.G., Chowrira,B., McSwiggen,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unknown
                                                                                                                                                                                                                                                                                          Method and reagent for inhibiting human
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                                                                                                                                                                                                                                                                                                                                       Unclassified.
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140 from patent US 5972704.
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Sequence 140 from patent
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12; Conserv
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AR060384
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Location/Qualifiers
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1 (bases 1 to 25)
Picoult-Newburg, L. and Pohl, M.
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synthetic construct
       Hodgkin's disease associated molecules Patent: US 5840568-A 6 24-NOV-1998; Location/Qualifiers
                                   1 (bases 1 to 27)
Pfreundschuh, M.
                                                                   Unknown
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ent: US 5693535-A 140 02-DEC-1997;
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                      l Similarity
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1 (bases 1 to 27)
1 (bases 1 to 27)
Pfreundschub, M.I.
Method for identifying or isolating a molecule and molecules indentified thereby
Patent: EP 1108432-A 6 20-JUN-2001;
LUDWIG INSTITUTE FOR CANCER RESEARCH (US)
                                                                                                                                                                                                                                                                                                                                                                           Similarity
12; Conserv
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Ffreundschuh, M. and Rammensee, H.

Nonapeptides that bind a HLA-A2.1 molecule
Patent: US 6140464-A 6 31-OCT-2000;
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Sequence 164 from Patent
AX155921
AX155921.1 GI:14537028
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Sequence 21 from patent
AR082956
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Voytas, D.F. and Zou, S.
Retrotransposon and methods
Patent: US 5976795-A 20 02-NOV-1999;
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Sequence 20 from patent US 5976795.
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Sammes, P.G. and Garman, A.J.
NUCLEIC ACID DETECTION WITH ENERGY TRANSFER
Patent: WO 9508642-A 3 30-MAR-1995;
ZENECA LTD (GB)
Ataxia-telangiectasia gene and its genomic organization Patent: US 5858661-A 25 12-JAN-1999;
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1 (bases 1 to 29)

Probst.P., Bhatia,A., Skeiky,Y.A., Fling,S.P. and Scholler,J.
Compounds and methods for treatment and diagnosis of chlamydial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Other publication AU 7662794 950410 Other publication GB 2283095 950426.
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Nucleic acid detection with energy transfer
Patent: US 5827653-A 3 27-OCT-1998;
Location/Qualifiers
1. 30
                                                                                                                                  Mutated forms of the ataxia-telangiectasia screen for a partial A-T phenotype Patent: US 6200749-A 104 13-MAR-2001;
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Sequence 104 from patent US
AR138579
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Sequence 3 from
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nilarity 100.0%; Pred. No.
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1 (bases 1 to 30)
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Sequence 22 from Patent
AX020976
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Location/Qualifiers
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AR140326
AR140326.1 GI:14482822
                                                                                                                                                                                                      cfre gene by arms Patent: EP 0928832-A 22 14-JUL-1999;
                                                                                                                                                                                                                               Kelly,S.J., Weston,S.L. and Robertson,N.H. Cystic fibrosis test based on the detection
                                                                                                                                                                                             ZENECA LTD (GB)
                                                                                                                                                                                                                                                                                          synthetic construct.
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milarity 100.0%;
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/db_xref="taxon:32630"
/note="PCR Amplification Primer"
/ note="PCR Amplification Primer"
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5 c 6 g
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0; Mismatches 0;
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                                                                                      Herrnstadt, C. and Davis, R.E. Single nucleotide polymorphisms in mitochondrial genes that segreg ate with alzheimer's disease Patent: WO 0063441-A 43 26-OCT-2000;
                                                                                                                                                          synthetic construct.
synthetic construct
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1 (bases 1 to 26)
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/db_xtef="taxon:32630"
/note="PCR primer"
/note="PCR primer"
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/note="synthetic oligonucleotide"
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                                                                                                                                        Mutated forms of the ataxia-telangiectasia gene and method screen for a partial A-T phenotype patent: US 6200749-A 158 13-MAR-2001;
Location/Qualifiers
                                                                                                                                                                                                                      Unknown
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Sequence 158 from patent US 6200749.
AR138633
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AR028230
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Shiloh, Y.
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New Helicobacter pylori antigens and related nucleic acid sequences - useful in serological diagnosis and protective vaccines, providing long-lasting immune response
                                                                                                                                                                                                i. youic cluster family; vaccine; gastritis; diagnosis; gastric adenocarcinoma; gastric lymphoma; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proteins that are characterised by immunoreactivity with H. pylori:positive antisera. The specification also describes 69 previously unrecognised immunogenic cluster families. H. pylori antigens are used to detect H. pylori-specific antibodies, for in vaccines to protect against H. pylori infection or to confirm eradication of infection, and diseases (gastritis, peptic ulcer, gastric adenocarcinoma/lymphoma). The present primer is used in the course of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           which describes Helicobacter pylori antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genome; biallelic marker; high density disequilibrium map; genomic map; haplotype; phenotype; polymorphic base; genotyping; haplotyping; hybridisation; identification; characterisation; diagnosis; single nucleotide polymorphism; SNP; ds.
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100.0%; Pred. No. 1e+03;
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Matches 16; Conserv
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                                                                                                            AAV90775;
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                                                                                                                                                                                             Antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This is a PCR primer used in the amplification of the Shigella dysenteriae I delta-stxA allele. The delta-stxA allele was integrated into delta-guab. A of delta-virG S. dysenteriae I, which inactivated the shiga toxin of this strain. The mutant can be used in shigella mutant, (which encodes and expresses a foreign antigen, and a shigella mutant, (which encodes and expresses a foreign antigen, and comprising the Shigella mutant (which also contains a plasmid which vaccines can be used against Shigellosis.
                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                            Delta-virG allele; delta-guaB-A allele; PCR; amplification; primer;
delta-stxA allele; shigellosis; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shigella mutants with mutation in guaB-A - used in vaccines against
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                                                                                                                         DB 20; Length 32; 1e+03;
                                                                                                                                                       Indels
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Pred. No. 1e+03;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                             Shigella dysenteriae delta-stxA allele PCR primer 13.
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                                                                                                                                                    Mismatches
                                                                                                                         Score 16;
Pred. No.
2005
                                                                                                                        4.>v,
100.0%; Prt
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100.0%; Pre
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                                                                                                                                                                                                                                                                         AAT97603 standard; DNA; 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96US-0629600
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                                                                                                                                                                          189 aaaataattatttta 204
                                                                                                                                                 Conservative
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                                                                                                   Shigella dysenteriae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-512417/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9737685-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Levine MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
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Gaps

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variation

Best Loca Matches

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AV90775 D AAV9(

RESULT

Length 39 Indels

д δ RESULT Query Match Best Local Similarity Thes 16; Conserve Matches Ş RESULT 밁 30-APR-1998 AAT97603 AAT97603 standard; DNA; This is a PCR primer used in the amplification of the Shigella dysenteriae I delta-stxA allele. The delta-stxA allele was integrated into delta-guab-A of delta-guab-A, delta-virG S. dysenteriae I, which inactivated the shiga toxin of this strain. The mutant can be used in the preparation of vaccines such as, a live vector vaccine comprising a Shigella mutant, (which encodes and expresses a foreign antigen, and a pharmaceutically acceptable carrier) or a DNA mediated vaccine comprising the Shigella mutant (which also contains a plasmid which encodes and expresses a foreign antigen in a eukaryotic cell). The vaccines can be used against Shigellosis. Shigella dysenteriae Synthetic. Delta-virG allele; delta-stxA allele; Shigella 09-APR-1997; WO9737685-Al 189 16-OCT-1997 Shigella mutants with mutation in guaB-A - used in vaccines against Levine MM, (UYMA-) UNIV MARYLAND BALTIMORE y Match 4.9%; Local Similarity 100.0%; hes 16; Conservative (Example 6; Page 57; 94pp; Shigellosis Sequence 36 189 aaaataattattttta 204 14 aaaataattatttta 19 aaaataattattttta 204 aaaataattatttta dysenteriae delta-stxA allele PCR primer Noriega FR; (first entry) ВP; Conservative 97WO-US05954 96US-0629600. 11 A; 3 C; delta-guaB-A allele; PCR; amplification; primer; shigellosis; vaccine; ss. 4.9%; 29 36 ВP English. 0; 10 G; 12 T; 0 other; 0 Score 16; Pred. No. Mismatches ore 16; DB 18; ored. No. 1e+03; Mismatches 0; Length 36 Indels 0 Gaps 0

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XEXEX
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                        The specification, which describes Helicobacter pylori antigenic proteins that are characterised by immunoreactivity with proteins that are characterised by immunoreactivity with pylori-positive antisera. The specification also describes 69 he pylori-positive immunogenic cluster families. H. pylori antigens are used to detect H. pylori-specific antibodies, for antigens are used to detect H. pylori-specific antibodies, for antigens infection or to confirm eradication of infection, and in vaccines to protect against H. pylori infection and related diseases (gastritis, peptic ulcer, gastric adenocarcinoma/lymphom The present primer is used in the course of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptic ulcer;
                                                                                                                                                                                                                                                                                                   Chow
                                                                                                                                                                                                                                                                                                                                                            14-OCT-1997;
25-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9849314-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antigen; imm
                                                                                                                                                                                                                                                                                                                                                                                                           27-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                        05-NOV-1998
                                                                                                                                                                           Claim Disclosure: Page 194; 402pp; English
                                                                                                                                                                                                                     New Helicobacter pylori antigens and related nucleic acid sequences useful in serological diagnosis and protective vaccines, providing
                                                                                                                                                                                                                                                                     WPI; 1999-009433/01
                                                                                                                                                                                                                                                                                                                             (GENE-) GENELABS TECHNOLOGIES
                                                                                                                                                                                                          long-lasting immune response
 Sequence 39
                                                                                                                                                                                                                                                                                                   TP,
                                                                                                                                                                                                                                                                                                    Fry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gastric cluster family; vaccine; gastritis; diagnosis; gastric adenocarcinoma; gastric lymphoma; primer; ss.
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                                                                                                                                                                                                                                                                                                                                                               97US-0061958
97US-0045107
                                                                                                                                                                                                                                                                                                                                                                                                           98WO-US08487
   15 A;
                                                                                                                                                                                                                                                                                                      Lim MY, McAtee CP:
    8 C;
      7 G; 9 T; 0 other;
                                                   gastric adenocarcinoma/lymphoma)
                                                                                                                                                                                                                                   providing
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Best

Query Match

Score 16; Pred. No.

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DB 20; 1e+03;

Length 32:

AAV90775;

0

Indels

0,

á Query Match Best Local S Matches 16 œ atatcttaaatttagc 23 1 Similarity 16; Conserv Conservative 4.9%; 0; Score Pred. Mismatches . No. DB 20; le+03; 0 Indels 0 Gaps

BP;

В 23 σ atatettaaatttage 38

RESULT AAZ68379 AAZ68379 AAZ68379 standard; DNA; 47

10-SEP-2001

(first entry)

Human genome: biallelic marker; high density disequilibrium m genomic map; haplotype; phenotype; polymorphic base; genotypi haplotyping; hybridisation; identification; characterisation; diagnosis; single nucleotide polymorphism; SNP; ds. Human map-related biallelic marker SEQ ID genotyping:

NO:2726

Homo sapiens

Key variation Location/Qualifiers replace(24,A)

AAV90775

AAV90775 standard; DNA; 39

0

Length 39

) lo Edenitege 1

(without alignments) 1261.226 Million cell updates/sec atttgggatatcttaaattt......tttcatgttttcttattgtt 327 January 24, 2002, 02:27:08 ; Search time 222.28 Seconds GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. Total number of hits satisfying chosen parameters: 930621.seqs, 428662619 residues OM nucleic - nucleic search, using sw model Gapext 60.0 US-09-531-438-3 OLIGO_NUC Gapop 60.0 , Minimum DB seq length: 0 Maximum DB seq length: 50 Title: Perfect score: Sequence: Scoring table: Word size : Searched: Run on:

AAT42655 RESULT

| SIDS2/gcddata/geneseq/geneseqr/NA1989.DAT:*
| SIDS2/gcgdata/geneseq/geneseqn/NA1980.DAT:*
| SIDS2/gcgdata/geneseq/geneseqn/NA1991.DAT:*
| SIDS2/gcgdata/geneseq/geneseqn/NA1992.DAT:*
| SIDS2/gcgdata/geneseq/geneseqn/NA1992.DAT:*

/SIDS2/gcgdata/geneseq/geneseqn/NA1982.DAT:*/SIDS2/gcgdata/geneseq/geneseqn/NA1983.DAT:*/SIDS2/gcgdata/geneseq/geneseqn/NA1984.DAT:*/SIDS2/gcgdata/geneseq/geneseqn/NA1985.DAT:*/SIDS2/gcgdata/geneseq/geneseqn/NA1986.DAT:*/SIDS2/gcgdata/geneseq/geneseqn/NA1986.DAT:*/SIDS2/gcgdata/geneseq/geneseqn/NA1986.DAT:*/SIDS2/gcgdata/geneseq/geneseqn/NA1986.DAT:*/SIDS2/gcgdata/geneseq/geneseqn/NA1986.DAT:*/SIDS2/gcgdata/geneseqn/NA1988

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Post-processing: Listing first 45 summaries

Database :

/SIDS2/gcgdata/geneseq/geneseqn/NA1994_DAT:*/SIDS2/gcgdata/geneseq/geneseqn/NA1995.DAT:*/SIDS2/gcgdata/geneseq/geneseqn/NA1996.DAT:*

/SIDS2/gcddata/geneseq/geneseqn/NA1997.DbT:*/SIDS2/gcgdata/geneseq/geneseqn/NA1998.DbT:*/SIDS2/gcgdata/geneseq/geneseqn/NA1090.DbT:*/SIDS2/gcgdata/geneseq/geneseqn/NA2000.DbT:*/SIDS2/gcgdata/geneseq/geneseqn/NA2001.DbT:*

ALIGNMENTS

25-FEB-1997 (first entry)

Primer for amplifying verotoxin (VT-1) subunit A coding sequence.

Verotoxin; Escherichia coli; enteric infection; diarrhoea; vaccine; haemolytic uraemic syndrome; detection; ss. 95US-0410058. 96WO-US04093 25-MAR-1996; WO9630043-A1 03-OCT-1996 Synthetic

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query Match Length DB

Score

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Stafford DC; Padhye NV, Carroll SB,

WPI; 1996-505779/50.

PCR primer for Ver Shigella dysenterly Primer Y104F Syn Human map-related

Primer for amplify

Description

primer

N-terminal

AAT42655 AAA51200 AA227689

AAT97603 AAV90775 AAZ68379 AAA66183

AAT39439 AAV37457 AAQ43975

AAH46804

20 20 20 20 21 22 17 119

Dog genomic marker Human high motilit Hel-N2 selected se Human Hel-N2 selec Triple helix formi

Compsn. contg. neutralising antitoxin against E.coli vero-toxin used to treat intoxicated individuals, and as a prophylactic against diarrhoeal disease or extra-intestinal complications of E.coli infection

AAT42655 standard; DNA; 29 BP AAT42655;

(OPHI-) OPHIBIAN PHARM INC 24-MAR-1995;

Cross-linking olig Cross-linking olig Oligomer HSV724 fo Oligomer HSV723 fo Human C-IAP-1 mRNA Human IQGAP2 CpG i Human IQGAP2 55-fata Helicobacter pylor Helicobacter pylor Primer for amplify N-terminal primer PCR primer for ver shipfile dysenter! Tomato spotted will Glycophorin antibo Oligonucleotide us Oligonucleotide TA Oligonucleotide TA Oligonucleotide TA Human gene signatu Nucleotide fragmen Human map-related Human map-related Human MSH6 fragmen Helicobacter pylor Human map-related Human map-related Renilla reniformis Human map-related Nucleotide IGFBP3 IGFBP3 IGFRP3 AAT42655 AAA51200 AAF55450 AAC88874 AA267533 AA267549 AA267813 AAA98312 AAF48097 AAF48098 1689 AAQ20160 AAQ30310 AAF55419 AAA57758 AAQ92084 AAS01643 AAV07922 AAQ62952 4AZ66366 AAT25703 AAV67854 AAC88875 AA267473 AAF48099 AAV07 AAA51 18 13 18 13 18 13 18 13 18 20 22 22 000 UQ

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Compositions containing neutralising antitoxin against one or more E. coli verotoxin (VT) can be used to treat intoxicated adults and children with enteric bacterial infections. They may also be used as children with enteric bacterial infections. They may also be used as prophylactics e.g. as a vaccine, against diarrhoeal disease or the prophylactics e.g. as a vaccine, against diarrhoeal disease or the prophylactic used to development of extra-intestinal complications of E. coli Infection, development of extra-intestinal complications of E. coli Infection, used to detect E. coli VT in a sample. The VT is recombinant, and the fusion protein containing a non-VT protein sequence and preferably a fusion protein containing a non-VT protein sequence and part of the E. coli VTI or VT2 sequence. Two primers (AAT42655, AAT42656) were used to amplify the verotoxin VT-1 A subunit coding sequence. Two primers (AAT42655, AAT42658) were used to amplify the verotoxin VT-1 A and B subunits and add a histidine tag coding to verotoxin VT-1 A and B subunits and add a histidine tag coding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.9%;
Justy 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP; 11 A; 2 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101pp; English
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     strict uninduced promoter control is necessary to permit cell viability. Strict uninduced promoter control is necessary to permit cell viability. Bacterial host cells expressing a recombinant expression vector encoding polyhistidine affinity tag and a portion of the VT-2 B chain are a polyhistidine affinity tag and a portion of the VT-2 B chain are permit the vector is chosen from per24hisVT2BL, per24hisVT2BL, and claimed. The vector is chosen from per24hisVT2BL, and "L-" indicates that the vector encodes the preprotein form of the protein and "L-" indicates that the vector encodes the mature form of the protein. The bacterial cell is capable of expressing large quantities (40 mg/1) of VT-2B. The toxins are useful for immunizing non-mammals and for detecting bacterial toxins in environmental samples including soil, water, industrial samples, biological samples and samples obtained from food and dairy processing instruments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to add the polyhistidine tag. The primers delete the native stop codons, and when cloned into pET-23 add a C-terminal extension of Leu-Glu-(His)6
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                                               This sequence represents a PCR primer of the invention. The primer used for amplification of the E. coli verotoxin (VT) gene. The oligonucleotide is useful for detection of inactivated VT gene by transfer of a foreign DNA fragment. Simple, rapid and specific amplification of VT gene from environmental factors is achieved us oligonucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Verotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCR primer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli
                                                                                                                                                                                                                                                                                                                            An oligonucleotide for amplification of verotoxin detection of inactivated verotoxin gene by transfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-FEB-1998;
                                                                                                                                                                                                                                             Claim 11;
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16; Conservative
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                                                                                                                                                                                                                                                  Page 9; 10pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VT1; VT2; detection; PCR primer:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.98;
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pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G; 11 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 21;
le+03;
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                                                                                                                                                                                                                                                                                                                                                  foreign DNA
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Sequence 32

BP; 12

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Gaps
                                                                                                                                                             Cross-linking oligomer 724 to target Herpes Simplex Virus I.
                                                                                                                                                                                 deoxyribonucleic acid; major groove; HSV;
inverted polarity region; covalent cross-linking group; ss
      Lengin 48;
                                                                                                                                                                                                                                                                                                               'note= "N-methyl-8-oxo-2'-deoxyadenine"
                                                                                                                                                                                                                                                                                                                                                   /note= "N-methyl-8-oxo-2'-deoxyadenine'
                                                                                                                                                                                                                                                                                                                                                                              /mod_base= OTHER
/note= "N-methyl-8-oxo-2'-deoxyadenine"
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/note= "N-methyl-8-oxo-2'-deoxyadenine"
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/note= "N-methyl-8-oxo-2'-deoxyadenine
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    ore 15; DB 15;
red. No. 2.5etC
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inverted_polarity_region
                                                                                                                                                                                                                                                                        'note= "N4N4-ethanocytosine"
                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "see comments
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/mod_base= OTHER
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/note= "N-methyl
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/mod_base= OTHER
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/mod_base= OTHER
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                                                                                                         BP.
                                                                                                    AAQ20161 standard; DNA; 18
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/label= j
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                                                                                                                                                                                                               Synthetic.
                                                                                                                        AAQ20161;
                                                                                  RESULT 13
AAQ20161
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Gaps
                                                                                                                                                                                                                                                                                                                                                                                      This oligomer contains an inverted polarity region formed from an 0-xyloso dimer synthon. Residues 11 and 12 are linked via an 0-xyloso group (i.e. nucleotides that have xylose sugar linked via the 0-xylene ring). The sequence is designed to target the Herpes Simplex virus I beginning at nucleotide 10996 and to covalently cross-link to it. See also AAQ20151-Q20160.
                                                                                                                                                                                                                                                                                                               New sequence-specific non-photo-activated crosslinking agents bind to the major groove of duplex DNA and are esp. useful for treating latent infections e.g. HIV
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  /note= "N-methyl-8-oxo-2'-deoxyadenine"
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                                                                         /*tag* n
/mod_base= OTHER
/note= "N-methyl-8-oxo-2/-deoxyadenine"
                                                  /note= "N-methyl-8-oxo-2'-deoxyadenine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.3%; Score 14; DB 13;
100.0%; Pred. No. 6.9e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18 BP; 12 A; 1 C; 0 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                Example 4; Page 29; 42pp; English.
                            /*tag= m
/mod_base= OTHER
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                                                                                                                                                                                                   91US-0640654.
                                                                                                                                                                                                                                                                 Krawczyk S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 4.3
Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                      (GILE-) GILEAD SCIE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159 aaaatataaataaa 172
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              modified_base
                                                           modified_base
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                                                                                                                                                                        24 - MAY - 1991;
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01,-APR-1992 (first entry) DNA; AAQ20160 standard; AAQ20160; REGULT 14 AMOZ0160

BP.

18

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oss-linking oligomer 723 to target Herpes Simplex Virus I. uss-linking ma or groove; uali/fiers Location/d coxyribonucleic acid; ma Synthet Key

ne∕hyl-8-oxo-2′-deoxyadenine" OTHER /tag= a note= "Nmodifi/ed_base mod Lied_base

/mod_base= OTHER /*tag=

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